
M P S R L H
(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:34:45 2000; MasPar time 7.31 Seconds
505.226 Million cell updates/sec

Tabular output not generated.

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pep
Perfect Score: 1078
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAEGPSDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 189963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:geneseq36
1:geneseq

Statistics: Mean 31.169; Variance 144.272; scale 0.216

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1078	100.0	156	1 R85116	Cell-cycle regulatory	1.18e-85
2	1067	99.0	156	1 W80524	A human multiple tumou	1.20e-84
3	1067	99.0	156	1 W40524	Human MTS1 protein.	1.20e-84
4	1067	99.0	156	1 W74549	Amino acid sequence of	1.20e-84
5	1067	99.0	156	1 W19251	Human multiple tumou	1.20e-84
6	1067	99.0	156	1 W10627	Tumour suppressor p16.	1.20e-84
7	1064	98.7	391	1 W95094	CDK inhibitory fusion p	2.26e-84
8	1064	98.7	391	1 W95094	CDK inhibitory fusion p	2.26e-84
9	1057	98.1	237	1 W95103	Truncated p27/p16 fusi	9.86e-84
10	1057	98.1	252	1 W95106	Truncated p27/p16 fusi	9.86e-84
11	1057	98.1	334	1 W95103	CDK inhibitory fusion	9.86e-84
12	1057	98.1	365	1 W95096	Human p16p27 fusion pr	9.86e-84
13	1057	98.1	365	1 W95107	Human p16p27 fusion pr	9.86e-84
14	1057	98.1	365	1 W95107	Human p16(GS)p27 fusi	9.86e-84
15	1057	98.1	380	1 W95095	CDK inhibitory fusion	9.86e-84
16	1057	98.1	380	1 W95095	CDK inhibitory fusion	9.86e-84
17	1056	98.0	156	1 W19252	Human multiple tumou	1.22e-83
18	1050	97.4	156	1 W19253	Human multiple tumou	4.31e-83
19	1037	96.2	348	1 W95104	Truncated p27/p16 fusi	6.65e-82
20	1030	95.5	148	1 R81701	Multiple tumour suppre	2.90e-81
21	1030	95.5	148	1 R80940	Human multiple tumou	2.90e-81
22	1030	95.5	151	1 R33401	Inhibitor of cyclin de	2.90e-81
23	921	85.4	157	1 R85114	Cell-cycle regulatory	2.59e-71

24	737	68.4	130	1 R85118	Cell-cycle regulatory	1.33e-54
25	735	68.2	105	1 W74550	Amino acid sequence 1	2.02e-54
26	735	68.2	105	1 R80947	Human multiple tumour	2.02e-54
27	735	68.2	105	1 W19254	Human MTS1E1-beta prot	2.02e-54
28	735	68.2	105	1 W40525	Human MTS1E1-beta prot	2.02e-54
29	735	68.2	105	1 R81700	Multiple tumour suppre	2.02e-54
30	735	68.2	105	1 W80525	A human multiple tumou	2.02e-54
31	729	67.6	130	1 W70823	Mouse multiple tumour	7.06e-54
32	725	67.3	138	1 R80948	Human multiple tumour	1.62e-53
33	725	67.3	138	1 W80526	A human multiple tumou	1.62e-53
34	725	67.3	138	1 R81702	Multiple tumour suppre	1.62e-53
35	725	67.3	138	1 W74553	Amino acid sequence 2	1.62e-53
36	725	67.3	138	1 W40526	Human MTS2 protein.	1.62e-53
37	725	67.3	138	1 W19255	Human multiple tumour	1.62e-53
38	713	66.1	138	1 R85117	Cell-cycle regulatory	1.97e-52
39	676	62.7	168	1 W80527	Mouse multiple tumour	4.31e-49
40	556	51.6	138	1 R85115	Cell-cycle regulatory	2.58e-38
41	484	44.9	67	1 W16324	Human INK4a-p16 C-term	6.67e-32
42	473	43.9	125	1 W16322	Murine INK4a-p16 C-ter	6.31e-31
43	473	43.9	125	1 R85120	Cell-cycle regulatory	6.31e-31
44	446	41.4	85	1 R85113	Cell-cycle regulatory	1.54e-28
45	446	41.4	127	1 R85119	Cell-cycle regulatory	1.54e-28

ALIGNMENTS

RESULT 1
ID R85116 standard; Protein; 156 AA.
AC R85116;
DT 01-MAR-1996 (first entry)
DE Cell-cycle regulatory protein p16.
KW Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
KW CCR; cancer; cell proliferation.
OS Homo sapiens.
PN WO9528483-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U046336.
PR 14-APR-1994; US-227371.
PR 25-MAY-1994; US-248812.
PR 14-SEP-1994; US-306511.
PR 29-NOV-1994; US-346147.
PA (COLD-) COLD SPRING HARBOR LAB.
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
DR MPI; 95-373798/48.
DR N-PSDB; T02962.

PT New cell cycle regulating proteins bind to cyclin dependent kinase -
and related nucleic acids, antibodies etc., used in diagnosis and
therapy of abnormal cell proliferation, degeneration etc.
PS Claim 1; Page 76-77; 109pp; English.
CC The human cell-cycle regulatory (CCR) protein p16 (R85116) was
obt'd. by expression of a cDNA clone (T02962) isolated in a 2-hybrid
screening assay. CCR p16 specifically inhibits the activity of
cyclin-dependent kinases during various stages of the cell cycle,
and can be used in the treatment and diagnosis of proliferative
disorders. 156 AA;
SQ Sequence 156 AA;

Query Match 100.0%; Score 1078; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.18e-85;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	MDPAGSSMEPSADWLATAAARGVEVRALLEAVALPAPNSYGRPIQVMGMSARVA	60
QY	1	MDPAGSSMEPSADWLATAAARGVEVRALLEAVALPAPNSYGRPIQVMGMSARVA	60
Db	61	ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRHAGARLDVDRGRLPVDLAE	120
QY	61	ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRHAGARLDVDRGRLPVDLAE	120
Db	121	LGHDRVARYLRAAAGGTGSGNHARIDAEGPSDIPD	156
QY	121	LGHDRVARYLRAAAGGTGSGNHARIDAEGPSDIPD	156

RESULT 2
 ID W80524 standard; Protein; 156 AA.
 AC W80524;
 DT 03-FEB-1999 (first entry)
 DE A human multiple tumour suppressor 1 (MTS1) protein.
 KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.
 OS Homo sapiens.
 PN US5843756-A.
 PD 01-DEC-1998.
 PE 28-JUL-1995; 058735.
 PR 28-JUL-1995; US-508735.
 PR 07-JUN-1995; US-487033.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Jiang P, Kamb A, Stone S;
 DR WPI: 99-044585/04.
 DR N-PSDB: V70583.
 PT Mouse multiple tumour suppressor gene segment - useful for primer design
 PS Disclosure: Columns 65-66; 80pp; English.
 CC The present sequence represents a human multiple tumour suppressor 1 (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
 SQ Sequence 156 AA;
 Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 1.20e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MEPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 QY 1 MDPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 Db 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
 QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
 RESULT 4
 ID W74549 standard; Protein; 156 AA.
 AC W74549;
 DT 04-DEC-1998 (first entry)
 DE Amino acid sequence of multiple tumour suppressor 1.
 KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
 KW Somatic mutation; gene therapy.
 OS Homo sapiens.
 PN US5801236-A.
 PD 01-SEP-1998.
 PE 07-JUN-1995; 480810.
 PR 07-JUN-1995; US-480810.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 14-APR-1994; US-215087.
 PR 01-JUN-1994; US-227369.
 PR 17-MAR-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI: 98-494842/42.
 DR N-PSDB: V53819.
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences - useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS mutation(s)
 PS Disclosure: Column 63-64; 73pp; English.
 CC This is the amino acid sequence of the multiple tumour suppressor 1 (MTS-1) protein, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can also be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell.
 SQ Sequence 156 AA;
 Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 1.20e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MEPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 QY 1 MDPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 Db 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
 QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
 RESULT 3
 ID W40524 standard; Protein; 156 AA.
 AC W40524;
 DT 15-JUL-1998 (first entry)
 DE Human MTS1 protein.
 KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition.
 OS Homo sapiens.
 PN US5739027-A.
 PD 14-APR-1998.
 PE 07-JUN-1995; 487033.
 PR 07-JUN-1995; US-487033.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI: 98-250421/22.
 DR N-PSDB: V11238.
 PT DNA specific for Multiple Tumour Suppressor 1el-beta gene - are useful for the diagnosis of cancers related to MTS1el-beta mutation(s) and their treatment
 PS Disclosure: Column 63-64; 72pp; English.
 CC This sequence represents a human multiple tumour suppression protein,

CC MTS1. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
 SQ Sequence 156 AA;

Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 1.20e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MEPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 QY 1 MDPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 Db 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
 QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 4
 ID W74549 standard; Protein; 156 AA.
 AC W74549;
 DT 04-DEC-1998 (first entry)
 DE Amino acid sequence of multiple tumour suppressor 1.
 KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
 KW Somatic mutation; gene therapy.
 OS Homo sapiens.
 PN US5801236-A.
 PD 01-SEP-1998.
 PE 07-JUN-1995; 480810.
 PR 07-JUN-1995; US-480810.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 14-APR-1994; US-215087.
 PR 01-JUN-1994; US-227369.
 PR 17-MAR-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI: 98-494842/42.
 DR N-PSDB: V53819.
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences - useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS mutation(s)
 PS Disclosure: Column 63-64; 73pp; English.
 CC This is the amino acid sequence of the multiple tumour suppressor 1 (MTS-1) protein, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can also be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell.
 SQ Sequence 156 AA;

Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 1.20e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MEPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 QY 1 MDPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60

Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 1.20e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MEPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 QY 1 MDPAAGSMPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60

Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120
 QY ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

Db 121 LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

QY LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

RESULT 5

ID W19251 standard; Protein; 156 AA.

AC W19251;

DT 10-SEP-1997 (first entry)

DE Human multiple tumour suppressor 1 gene product.

KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.

OS Homo sapiens.

PN US5624819-A.

PD 29-APR-1997.

PF 18-MAR-1994; 214582.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PR 17-MAR-1995; WO-003537.

PR 07-JUN-1995; US-474177.

PA (MYRI-) MYRIAD GENETICS INC.

PA (UTAH) UNIV UTAH RES FOUND.

PI Cannon-Albright LA, Kamb A, Skolnick MH;

DR WPI: 97-258217/23.

DR N-PSDB; T72311.

PT Human mutant multiple tumour suppressor gene sequences - for

PS production of recombinant mutant polypeptide(s)

PS Claim 1; Columns 61-64; 72pp; English.

CC The present sequence the human multiple tumour suppressor 1

CC (MTS1) gene product, useful in cancer diagnosis.

SQ Sequence 156 AA;

Query Match 99.0%; Score 1067; DB 1; Length 156;

Best Local Similarity 98.7%; Pred. No. 1.20e-84;

Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MEPAAGSMPEPSADWLATAAARGVEEVALLLEAGALPNAPNSYGRPIQVMMGMSARVA 60

QY 1 MDPAAGSMPEPSADWLATAAARGVEEVALLLEAGALPNAPNSYGRPIQVMMGMSARVA 60

Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

QY ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

Db 121 LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

QY LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

RESULT 6

ID W10627 standard; Protein; 156 AA.

AC W10627;

DT 28-OCT-1997 (first entry)

DE Tumour suppressor p16

KW Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;

KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;

KW anti-angiogenic activity; hyperproliferative disorder.

OS Homo sapiens.

PN WO9703635-A2.

PD 06-FEB-1997.

PF 17-JUL-1996; U11787.

PR 17-JUL-1995; US-502881.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Jin X, Roth J;

DR WPI: 97-132336/12.

DR N-PSDB; T60951.

PT Expression construct contg. DNA for tumour suppressor p16 - to
 PT restore p16 activity to transformed cells, useful for treating lung
 PT or bladder cancer or melanoma
 PS Disclosure; Fig 1b; 92pp; English.
 CC This sequence represents the tumour suppressor p16. The DNA encoding
 CC this sequence is joined to a promoter functional in eukaryotic cells and
 CC used in the expression construct of the invention. p16 is an inhibitory
 CC subunit, which is involved in the control of cyclin-dependent kinase 4
 CC activity, and functions as a tumour suppressor. By detecting this
 CC sequence or the DNA encoding it, cancer cells can be detected. When the
 CC nucleic acid molecule is in the sense orientation, the expression
 CC construct can be used to restore p16 function in a cell, particularly by
 CC reversing the transformed phenotype in tumours, especially lung or
 CC bladder cancer or melanoma. It may also have anti-angiogenic activity,
 CC and inhibit hyperproliferative disorders, e.g. restenosis. When the
 CC nucleic acid molecule is inserted in the antisense orientation, the
 CC expression construct inhibits p16 function. Reduced or increased levels
 CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by
 CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
 CC or immunoassay.
 SQ Sequence 156 AA;

Query Match 99.0%; Score 1067; DB 1; Length 156;

Best Local Similarity 98.7%; Pred. No. 1.20e-84;

Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MEPAAGSMPEPSADWLATAAARGVEEVALLLEAGALPNAPNSYGRPIQVMMGMSARVA 60

QY 1 MDPAAGSMPEPSADWLATAAARGVEEVALLLEAGALPNAPNSYGRPIQVMMGMSARVA 60

Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

QY ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

Db 121 LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

QY LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

RESULT 7

ID W95094 standard; Protein; 391 AA.

AC W95094;

DT 25-MAY-1999 (first entry)

DE Human p27-p16 fusion protein.

KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;

KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;

KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;

KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;

KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;

KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;

KW tachycardia; human; p27; p16.

OS Homo sapiens.

PN WO9906540-A2.

PD 11-FEB-1999.

PF 29-JUL-1998; U15759.

PR 29-JUL-1997; US-902572.

PA (MITO-) MITOTIX INC.

PI Beach DH, Gyuris J, Lamphere L;

DR WPI: 99-153770/13.

DR N-PSDB; X26220.

PT Fusion and chimaeric proteins including cyclin-dependent kinase

PT binding motif - used for regulation of cell proliferation and

PT differentiation, for treatment of, e.g. vascular injury, cancers,

PT fibrosis and neurodegeneration

PS Claim 63; Page 70-72; 88pp; English.

CC The invention relates to novel inhibitors of cyclin-dependent kinases

CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant

CC transfection system (A) that comprises: (i) first gene construct

CC comprising a sequence encoding an inhibitory polypeptide containing at

CC least one CDK-binding motif for binding and inhibiting activity of a CDK,

CC linked to a transcription regulator functional in eukaryotic cells; (ii)

CC second gene construct comprising a sequence encoding a polypeptide that

CC promotes endothelialisation, and (iii) a gene delivery composition for

CC delivering the GCs to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (TP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell, and (ii) a transcellular
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
 CC consists of at least one CDK-binding motif and a TCP. (A) are used to
 CC treat vascular wounds that involve a break in the endothelium and
 CC excessive proliferation of smooth muscle, particularly restenosis but
 CC more generally any repair of cardiovascular damage, arteriosclerotic
 CC lesions or for endothelialisation of synthetic vascular grafts. More
 CC generally, FP are used to treat unwanted cellular proliferation in a very
 CC wide range of situations, e.g. for treating vascular diseases as above;
 CC fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many
 CC tumours (gliomas, leukaemias); chronic inflammation; neurodegeneration;
 CC acne; also to control hair growth (e.g. to prevent hair loss caused by
 CC chemotherapy or radiation); periodontal disease; to treat tachycardia;
 CC to inhibit spermatogenesis etc. Chimaeric proteins comprising CDK-binding
 CC motifs from two or more different proteins bind to CDKs so inhibit cell
 CC cycle progression, particularly smooth muscle cell proliferation. The
 CC gene constructs may also be used to produce FP in cell cultures, for
 CC production or for regulating cell differentiation in vitro. The present
 CC sequence represents a human p27-p16 fusion protein.
 SQ Sequence 391 AA;

Query Match 98.7%; Score 1064; DB 1; Length 391;
 Best Local Similarity 98.7%; Pred. No. 2.26e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 236 MORAAGSMPEPSADWLATAAARGVEEVRALLEVALPNAPNSYGRPIQVMMGSRVA 295
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALLEVALPNAPNSYGRPIQVMMGSRVA 60
 Db 296 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVLHRRAGARLDVRDANGRLPVDLAE 355
 QY 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVLHRRAGARLDVRDANGRLPVDLAE 120
 Db 356 LGRDVARYLRAAGGTRGSHNARIDAAGPSDIPD 391
 QY 121 LGRDVARYLRAAGGTRGSHNARIDAAGPSDIPD 156

RESULT 8
 ID W3534 standard; Protein; 391 AA.

AC W3534;
 DT 16-MAR-1998 (first entry)
 DE CDK inhibitory fusion protein #1.
 KW Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;
 KW chimeric polypeptide; human; binding motif; proliferation control;
 KW cell differentiation; cell-cycle inhibitor; proliferative disorder;
 KW tissue degeneration; therapy.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 1..7
 FT Misc_difference 205..219 /note= "poly-His tag"
 FT Misc_difference /note= "(Gly/Ser)2 linker"

FN W09727297-A1.
 PD 31-JUL-1997.
 PF 17-JAN-1997; U00569.
 PR 23-JAN-1996; US-589981.
 PA (MITO-) MITOTIX INC.
 PI Beach D, Gyuris J, Lamphere L;
 DR WPI; 97-393685/36.
 DR N-PSDB; T74051.
 PT Chimeric inhibitor of cyclin dependent kinase - useful for gene
 PT therapy of cancer and other proliferative and differentiative
 PT diseases
 PS Claim 40; Page 38-40; 58pp; English.
 CC This sequence represents a chimeric polypeptide of the invention. It was
 CC derived from a fusion of the human p27 and p16 cDNA sequences. The
 CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)
 CC binding motifs from at least two different proteins that bind to CDKs.
 CC The protein controls proliferation and/or differentiation of cells,

CC particularly they inhibit cell-cycle progression. They can be used to
 CC treat a wide range of proliferative disorders, e.g. cancer, leukaemia,
 CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They
 CC can also treat diseases associated with de-differentiation or
 CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's
 CC diseases, gastric ulcers and autonomous diseases of the peripheral
 CC nervous system. Other applications include reducing growth of hair and
 CC protecting hair follicle cells against cytotoxic treatments, cosmetically
 CC to treat various forms of folliculitis, and to inhibit spermatogenesis or
 CC oogenesis. The chimeric proteins can also be used in vitro to maintain
 CC cells, especially neurons intended for testing specific activity of
 CC trophic factors, at selected points in the cell cycle. The proteins are
 CC more active inhibitors of the CDK/cyclin complex than binding motifs used
 CC individually (since they may bind to CDK involved in different stages of
 CC the cell cycle).
 SQ Sequence 391 AA;

Query Match 98.7%; Score 1064; DB 1; Length 391;
 Best Local Similarity 98.7%; Pred. No. 2.26e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 236 MORAAGSMPEPSADWLATAAARGVEEVRALLEVALPNAPNSYGRPIQVMMGSRVA 295
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALLEVALPNAPNSYGRPIQVMMGSRVA 60
 Db 296 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVLHRRAGARLDVRDANGRLPVDLAE 355
 QY 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVLHRRAGARLDVRDANGRLPVDLAE 120
 Db 356 LGRDVARYLRAAGGTRGSHNARIDAAGPSDIPD 391
 QY 121 LGRDVARYLRAAGGTRGSHNARIDAAGPSDIPD 156

RESULT 9

ID W95105 standard; Protein; 237 AA.

AC W95105;
 DT 25-MAY-1999 (first entry)
 DE Truncated p27/p16 fusion protein.
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 KW tachycardia; human; p27; p16; truncated.

OS Homo sapiens.

PN W0906540-A2.

PD 11-FEB-1999.

PF 29-JUL-1998; U15759.

PR 29-JUL-1997; US-902572.

PA (MITO-) MITOTIX INC.

PI Beach D, Gyuris J, Lamphere L;

DR WPI; 99-153770/13.

DR N-PSDB; X26233.

PT Fusion and chimaeric proteins including cyclin-dependent kinase
 PT binding motif - used for regulation of cell proliferation and
 PT differentiation, for treatment of, e.g. vascular injury, cancers,
 PT fibrosis and neurodegeneration
 PS Claim 63; Page 85; 88pp; English.

CC The invention relates to novel inhibitors of cyclin-dependent kinases
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 CC transfection system (A) that comprises: (i) first gene construct
 CC comprising a sequence encoding an inhibitory polypeptide containing at
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)
 CC second gene construct comprising a sequence encoding a polypeptide that
 CC promotes endothelialisation, and (iii) a gene delivery composition for
 CC delivering the GCs to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (TP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell, and (ii) a transcellular
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP

CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a human truncated p27/p16 fusion protein.
SQ Sequence 237 AA;

Query Match 98.1%; Score 1057; DB 1; Length 237;
Best Local Similarity 99.4%; Pred. No. 9.86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 83 DPAAGSMPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSAARVAE 142
QY 2 DPAAGSMPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSAARVAE 61

Db 143 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDAGRLPVDLAEEL 202
QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDAGRLPVDLAEEL 121

Db 203 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 237
QY 122 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 10
ID W95106 standard; Protein; 252 AA.
AC W95106;
DE 25-MAY-1999 (first entry)
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16; truncated.
OS Homo sapiens.
PN W09906540-A2.
PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; US-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI: 99-153770/13.
DR N-PSDB: X26234.
PT Fusion and chimeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 63; Page 85; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence 252 AA;

Query Match 98.1%; Score 1057; DB 1; Length 252;
Best Local Similarity 99.4%; Pred. No. 9.86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 98 DPAAGSMPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSAARVAE 157
QY 2 DPAAGSMPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSAARVAE 61

Db 158 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDAGRLPVDLAEEL 217
QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDAGRLPVDLAEEL 121

Db 218 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 252
QY 122 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 11
ID W95103 standard; Protein; 334 AA.
AC W95103;
DE 25-MAY-1999 (first entry)
KW Truncated p27/p16 fusion protein.
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16; truncated.
OS Homo sapiens.
PN W09906540-A2.
PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; US-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI: 99-153770/13.
DR N-PSDB: X26231.
PT Fusion and chimeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 63; Page 83; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence 334 AA;

Query Match 98.1%; Score 1057; DB 1; Length 334;
Best Local Similarity 99.4%; Pred. No. 9.86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 180 DPAAGSMPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSAARVAE 239
QY 2 DPAAGSMPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSAARVAE 61

Db 240 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDAGRLPVDLAEEL 299
QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDAGRLPVDLAEEL 121

Db 300 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 334
QY 122 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 12
ID W23536 standard; Protein; 365 AA.

CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a human p16p27 fusion protein.
SQ Sequence 365 AA;

Query Match 98.1%; Score 1057; DB 1; Length 365;
Best Local Similarity 99.4%; Pred. No. 9.86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 211 DPAAGSSMEPSADWLATAAAARGVVEVRLLEAGALPNAPNSYGRRPDIQYMMGMSARVAE 270
QY 2 DPAAGSSMEPSADWLATAAAARGVVEVRLLEAGALPNAPNSYGRRPDIQYMMGMSARVAE 61
Db 271 LLLHGAEPNCADPATLTRPVHDAAREGFDLTLLVLRAGARLDVRDAGRLPVDLAEEL 330
QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFDLTLLVLRAGARLDVRDAGRLPVDLAEEL 121
Db 331 GHRDVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 365
QY 122 GHRDVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 156

RESULT 15
ID W95095 standard; Protein; 380 AA.
AC W95095;
DT 25-MAY-1999 (first entry)
DE Human p16(GS)p27 fusion protein.
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16.
OS Homo sapiens.
PN WO9906540-A2.
PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; US-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI: 99-153770/13.
DR N-PSDB; X26223.
PT Fusion and chimaeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 63; Page 74-76; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular

CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a human p16(GS)p27 fusion protein.
SQ Sequence 380 AA;
Query Match 98.1%; Score 1057; DB 1; Length 380;
Best Local Similarity 99.4%; Pred. No. 9.86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 12 DPAAGSSMEPSADWLATAAAARGVVEVRLLEAGALPNAPNSYGRRPDIQYMMGMSARVAE 71
QY 2 DPAAGSSMEPSADWLATAAAARGVVEVRLLEAGALPNAPNSYGRRPDIQYMMGMSARVAE 61
Db 72 LLLHGAEPNCADPATLTRPVHDAAREGFDLTLLVLRAGARLDVRDAGRLPVDLAEEL 131
QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFDLTLLVLRAGARLDVRDAGRLPVDLAEEL 121
Db 132 GHRDVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 166
QY 122 GHRDVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 156

Search completed: Thu Jul 20 08:34:54 2000
Job time : 9 secs.

W P E R L H (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:36:50 2000; MasPar time 5.60 Seconds
401.877 Million cell updates/sec
Tabular output not generated.

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pep
Perfect Score: 1078
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAEAGSPDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 29.074; Variance 136.818; scale 0.212

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description	Pred. No.
1	1078	100.0	156	4 PCT-US95-0 Sequence 2, Applicatio	4.93e-85
2	1078	100.0	156	3 US-08-581- Sequence 2, Applicatio	4.93e-85
3	1078	100.0	156	2 US-08-306- Sequence 2, Applicatio	4.93e-85
4	1078	100.0	156	2 US-08-893- Sequence 2, Applicatio	4.93e-85
5	1078	100.0	156	2 US-08-627- Sequence 2, Applicatio	4.93e-85
6	1067	99.0	156	1 US-08-480- Sequence 2, Applicatio	4.84e-84
7	1067	99.0	156	2 US-08-486- Sequence 2, Applicatio	4.84e-84
8	1067	99.0	156	1 US-08-848- Sequence 2, Applicatio	4.84e-84
9	1067	99.0	156	2 US-08-487- Sequence 2, Applicatio	4.84e-84
10	1067	99.0	156	3 US-08-508- Sequence 2, Applicatio	4.84e-84
11	1067	99.0	156	2 US-09-120- Sequence 2, Applicatio	4.84e-84
12	1067	99.0	156	1 US-08-474- Sequence 2, Applicatio	4.84e-84
13	1067	99.0	157	4 PCT-US96-0 Sequence 5, Applicatio	4.84e-84
14	1064	98.7	391	1 US-08-589- Sequence 2, Applicatio	9.03e-84
15	1030	95.5	148	4 PCT-US93-0 Sequence 4, Applicatio	1.05e-80
16	1030	95.5	148	3 US-08-384- Sequence 16, Applicati	1.05e-80
17	1030	95.5	148	3 US-08-384- Sequence 24, Applicati	1.05e-80
18	1030	95.5	148	1 US-08-154- Sequence 12, Applicati	1.05e-80
19	921	85.4	157	3 US-08-581- Sequence 8, Applicatio	6.75e-71
20	737	68.4	130	4 PCT-US95-0 Sequence 8, Applicatio	2.05e-54
21	737	68.4	130	2 US-08-627- Sequence 8, Applicatio	2.05e-54
22	737	68.4	130	3 US-08-581- Sequence 8, Applicatio	2.05e-54
23	735	68.2	105	3 US-09-120- Sequence 14, Applicati	3.09e-54

24	735	68.2	105	1 US-08-480- Sequence 14, Applicati	3.09e-54
25	735	68.2	105	1 US-08-474- Sequence 14, Applicati	3.09e-54
26	735	68.2	105	1 US-08-487- Sequence 14, Applicati	3.09e-54
27	735	68.2	105	2 US-08-848- Sequence 14, Applicati	3.09e-54
28	735	68.2	105	2 US-08-486- Sequence 14, Applicati	3.09e-54
29	735	68.2	105	2 US-08-508- Sequence 14, Applicati	3.09e-54
30	729	67.6	130	2 US-08-508- Sequence 47, Applicati	1.06e-53
31	725	67.3	138	4 PCT-US95-0 Sequence 4, Applicatio	2.42e-53
32	725	67.3	138	3 US-08-384- Sequence 25, Applicati	2.42e-53
33	725	67.3	138	2 US-08-627- Sequence 4, Applicatio	2.42e-53
34	725	67.3	138	1 US-08-474- Sequence 16, Applicati	2.42e-53
35	725	67.3	138	1 US-08-487- Sequence 16, Applicati	2.42e-53
36	725	67.3	138	1 US-08-480- Sequence 16, Applicati	2.42e-53
37	725	67.3	138	2 US-08-486- Sequence 16, Applicati	2.42e-53
38	725	67.3	138	2 US-08-508- Sequence 16, Applicati	2.42e-53
39	725	67.3	138	3 US-09-120- Sequence 16, Applicati	2.42e-53
40	725	67.3	138	2 US-08-848- Sequence 16, Applicati	2.42e-53
41	725	67.3	138	3 US-08-581- Sequence 4, Applicatio	2.42e-53
42	682	63.3	136	4 PCT-US96-0 Sequence 6, Applicatio	1.64e-49
43	682	63.3	137	2 US-08-893- Sequence 4, Applicatio	1.64e-49
44	682	63.3	137	2 US-08-306- Sequence 4, Applicatio	1.64e-49
45	676	62.7	168	2 US-08-508- Sequence 46, Applicati	5.61e-49

ALIGNMENTS

RESULT 1
ID PCT-US95-04636-2 STANDARD: PRT: 156 AA.
XX
AC
XX
XX
DT

Sequence 2, Application PC/TUS9504636
Sequence 2, Application PC/TUS9504636
GENERAL INFORMATION:
APPLICANT:

TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii(text)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04636

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 156 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 156 AA; 16560 MW; 98948 CN;

Query Match 100.0%; Score 1078; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.93e-85;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 156 AA; 16560 MW; 98948 CN;

Query Match 100.0%; Score 1078; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 4,938-85;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDPAGSSMEPSADWLATAAAAGRVVEVRALEVALPNAPNSYGRRPDIQVMMGSAVA 60
|||||
Qy 1 MDPAGSSMEPSADWLATAAAAGRVVEVRALEVALPNAPNSYGRRPDIQVMMGSAVA 60
|||||

Db 61 ELLLLHGAEPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVDAWGRLPVDLAE 120
|||||
Qy 61 ELLLLHGAEPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVDAWGRLPVDLAE 120
|||||

Db 121 LGRDVARYLRAAGGTGSGNHARIDAAEGPSDIPD 156
|||||
Qy 121 LGRDVARYLRAAGGTGSGNHARIDAAEGPSDIPD 156
|||||

Sequence 2, Application US/08893274
Sequence 2, Application US/08893274
Patent No. 5968821
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOVEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/963,308
CC FILING DATE: 16-OCTOBER-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Vincent, Matthew P.
CC REGISTRATION NUMBER: 36,709
CC REFERENCE/DOCKET NUMBER: MIV-071.09
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 832-1000
CC TELEFAX: (617) 832-7000
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 156 AA; 16560 MW; 98948 CN;

Query Match 100.0%; Score 1078; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 4,938-85;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDPAGSSMEPSADWLATAAAAGRVVEVRALEVALPNAPNSYGRRPDIQVMMGSAVA 60
|||||
Qy 1 MDPAGSSMEPSADWLATAAAAGRVVEVRALEVALPNAPNSYGRRPDIQVMMGSAVA 60
|||||

Db 61 ELLLLHGAEPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVDAWGRLPVDLAE 120
|||||
Qy 61 ELLLLHGAEPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVDAWGRLPVDLAE 120
|||||

Db 121 LGRDVARYLRAAGGTGSGNHARIDAAEGPSDIPD 156
|||||
Qy 121 LGRDVARYLRAAGGTGSGNHARIDAAEGPSDIPD 156
|||||

RESULT 5
ID US-08-627-610-2 STANDARD; PRT; 156 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 2, Application US/08627610
XX
CC Sequence 2, Application US/08627610
CC Patent No. 5919997
CC GENERAL INFORMATION:
CC APPLICANT: Beach, David H.
CC APPLICANT: Serrano, Manuel
CC APPLICANT: Depinbo, Ronald A.
CC TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
CC TITLE OF INVENTION: Regulation
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: LAHIVE & COCKFIELD
CC STREET: 60 State Street
CC CITY: Boston
CC STATE: MA
CC COUNTRY: USA
CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: ASCII(text)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/627,610
CC FILING DATE: 04-APR-1996
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Vincent, Matthew P.
CC REGISTRATION NUMBER: 36,709
CC REFERENCE/DOCKET NUMBER: CSI-001CP6
CC TELECOMMUNICATION INFORMATION:

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CC TELEPHONE: (617) 227-7400
CC TELEFAX: (617) 227-5941
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 156 AA; 16560 MW; 98948 CN;

Query Match 100.0%; Score 1078; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 4,938-85;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDPAGSSMEPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRRPITQVMMGSAVA 60
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRRPITQVMMGSAVA 60

Db 61 ELLLLHGAEPNCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
QY 61 ELLLLHGAEPNCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120

Db 121 LGHRDVARYLRAAGTGRGSHARIDAAEGPSDIPD 156
QY 121 LGHRDVARYLRAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 6
ID US-08-480-810-2 STANDARD; PRT; 156 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 2, Application US/08480810
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XX Sequence 2, Application US/08480810
CC Patent No. 5801236
CC GENERAL INFORMATION:
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS1 GENE
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/480,810
CC FILING DATE: 07-JUN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/03316
CC FILING DATE: 17-MAR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,087
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,086
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC

CC TELEPHONE: (617) 227-7400
CC TELEFAX: (617) 227-5941
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 156 AA; 16532 MW; 98534 CN;

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Best Local Similarity 98.7%; Pred. No. 4,848-84;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 61 ELLLLHGAEPNCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120

Db 121 LGHRDVARYLRAAGTGRGSHARIDAAEGPSDIPD 156
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RESULT 7
ID US-08-486-047-2 STANDARD; PRT; 156 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 2, Application US/08486047
XX
XX Sequence 2, Application US/08486047
CC Patent No. 5994095
CC GENERAL INFORMATION:
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS2 GENE
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/486,047
CC FILING DATE: 07-JUN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/03316
CC FILING DATE: 17-MAR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC
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ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE: 156 AA: 16532 MW: 98534 CN:

Sequence 2, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/508,735
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 156 AA: 16532 MW: 98534 CN:

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QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLLHRAGARLDVRDANGRLPVDLAE 120
Db 121 LGHRDVARYLRAAGGTRGSNHARIDAAEGPSDIPD 156
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QY 121 LGHRDVARYLRAAGGTRGSNHARIDAAEGPSDIPD 156

RESULT 13
ID PCT-US96-05252-5 STANDARD; PRT; 157 AA.
XX AC xxxxxx
XX DT
XX DE
XX DE
XX DE
XX DE

Sequence 5, Application PC/TUS9605252

Sequence 5, Application PC/TUS9605252

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: p19: A Cell Cycle Inhibitor

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Tower

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/05252

FILING DATE: Not yet assigned

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,093

FILING DATE: 17-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen L. 32,762

REGISTRATION NUMBER: 02307B-059910PC

REFERENCE/DOCKET NUMBER: 02307B-059910PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..157

OTHER INFORMATION: /note= "human.p16"

SEQUENCE 157 AA; 16674 MW; 100395 CN;

Query Match 99.0%; Score 1067; DB 4; Length 157;

Best Local Similarity 99.4%; Pred. No. 4.84e-84;

Matches 156; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPPIQVMMGSAVA 60

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QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPPIQVMMGSAVA 60

|||||

Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLLHRAGARLDVRDANGRLPVDLAE 120

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QY 61 ELLLL-HGAEPNCADPATLTRPVHDAAREGFLDTLVLLHRAGARLDVRDANGRLPVDLAE 119

Db 121 ELGHRDVARYLRAAGGTRGSNHARIDAAEGPSDIPD 157
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QY 120 ELGHRDVARYLRAAGGTRGSNHARIDAAEGPSDIPD 156

RESULT 14
ID US-08-589-981-2 STANDARD; PRT; 391 AA.
XX AC xxxxxx
XX DT
XX DE
XX DE
XX DE

Sequence 2, Application US/08589981

Sequence 2, Application US/08589981

Patent No. 5672508

GENERAL INFORMATION:

APPLICANT: Gyuris, Jen

APPLICANT: Lamphere, Lou

TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,

TITLE OF INVENTION: and Uses Related Thereto

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/589,981

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MII-069

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 391 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 391 AA; 42306 MW; 652242 CN;

Query Match 98.7%; Score 1064; DB 1; Length 391;

Best Local Similarity 98.7%; Pred. No. 9.03e-84;

Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPPIQVMMGSAVA 60

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Db 296 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLLHRAGARLDVRDANGRLPVDLAE 355

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QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLLHRAGARLDVRDANGRLPVDLAE 120

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Db 356 LGHRDVARYLRAAGGTRGSNHARIDAAEGPSDIPD 391

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QY 121 LGHRDVARYLRAAGGTRGSNHARIDAAEGPSDIPD 156

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RESULT 15
ID PCT-US93-09945-4 STANDARD; PRT; 148 AA.

W P S R L H

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:35:12 2000; MasPar time 11.77 Seconds
625.481 Million cell updates/sec

Tabular output not generated.

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pep
Perfect Score: 1078
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHRIDAAEGPSDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pif63
1:pif1 2:pif2 3:pif3 4:pif4

Statistics: Mean 43.845; Variance 94.938; scale 0.462

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Pred. No.	
Result No.	Score	Query Match	Length	ID	Description	
1	1067	99.0	156	2 JE0141	cyclin dependent kina	3.86e-175
2	729	67.6	130	2 I78845	p15INK4b - mouse	1.59e-110
3	725	67.3	138	2 B55479	CDK4 inhibitor p14(IN	9.09e-110
4	663	61.5	167	2 I59352	p16INK4a - mouse	4.46e-98
5	353	32.7	164	2 A57378	cyclin-dependent kina	3.82e-41
6	341	31.6	166	2 A57378	CDK4/CDK6 inhibitor p	5.04e-39
7	338	31.4	166	2 B57378	cyclin-dependent kina	1.70e-38
8	300	27.8	168	2 A55479	CDK6 inhibitor p18 -	7.29e-32
9	292	27.1	168	2 B57379	CDK4/CDK6 inhibitor p	1.75e-30
10	284	26.3	41	2 I52720	gene p15INK4B protein	4.14e-29
11	181	16.8	3924	2 S37431	ankyrin 2, neuronal 1	3.58e-12
12	174	16.1	1856	2 B35049	ankyrin 1, erythrocyt	4.30e-11
13	174	16.1	1880	2 A35049	ankyrin 1, erythrocyt	4.30e-11
14	174	16.1	1881	1 SJHUK	ankyrin 1, erythrocyt	4.30e-11
15	173	16.0	1848	2 S37771	ankyrin, erythrocyte	6.11e-11
16	173	16.0	1862	2 I49502	ankyrin - mouse	6.11e-11
17	165	15.3	4377	2 A55575	ankyrin 3, long splic	1.00e-09
18	160	14.8	1786	2 A57282	ankyrin-related prote	5.64e-09
19	160	14.8	1809	2 T15345	ankyrin-related unc-4	5.64e-09
20	160	14.8	1815	2 T15346	elegans ankyrin-relat	5.64e-09
21	160	14.8	1867	2 T15344	ankyrin-related relat	5.64e-09
22	160	14.8	2039	2 T15347	ankyrin-related unc-4	5.64e-09
23	152	14.1	1349	2 T13940	ankyrin - fruit fly (8.61e-08


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GENETICS
#map_position 19p13
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankylrin
repeat homology; EGF homology
SUMMARY #length 164 #molecular-weight 17362 #checksum 5271

Query Match 32.78; Score 353; DB 2; Length 164;
Best Local Similarity 50.08; Pred.No.3.82e-41;
Matches 60; Conservative 19; Mismatches 39; Indels 2; Gaps 2;

Db 11 LSGAARGDVOEVRLLHRELHPHDALNRFKKTALQVMMFGSTAIALELLKOGASPNVD 70
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Qy 16 LATAAAGRVEEVALLL-AVALPNAAPNSVGRRPIQVMGMGSAARVAELLLLHGAEPCAD 74
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Db 71 TSG-TSPVHDAARTGTDLTKLVLRHGADVNPDPGTGALPIHLAVOEGHTAVVVFSLAES 129
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RESULT 6
ENTRY A57379 #type complete
TITLE CDK4/CDK6 inhibitor p19 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
20-Sep-1999
ACCESSIONS A57379
REFERENCE Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J.
#journal Mol. Cell. Biol. (1995) 15:2672-2681
#title Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.
#crosso-references PMID:95257948
#accession A57379
#status preliminary
#molecule_type mRNA
#residues 1-166 #label HIR
#crosso-references GB:U19597; NID:g790568; PIDN:AACS2194.1; PID:g790569
CLASSIFICATION #superfamily unassigned ankylrin repeat proteins; ankylrin
repeat homology; EGF homology
KEYWORDS cell cycle control
SUMMARY #length 166 #molecular-weight 17894 #checksum 3512

Query Match 31.68; Score 341; DB 2; Length 166;
Best Local Similarity 49.68; Pred.No.5.04e-39;
Matches 59; Conservative 19; Mismatches 39; Indels 2; Gaps 2;

Db 9 GDRLSGARAGDVOEVRLLHRELHPHDALNRFKKTALQVMMFGSPAVALLELLKOGASPN 68
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Db 69 VQDASG-TSPVHDAARTGTDLTKLVLRHGADVNDTGLSPIHLAIREGHSVVVSFL 136
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Qy 72 CADPATLTRPVHDAAREGFLDTLVLLHRAGARLDVRDANGRLPVDLAELGHDRDVARYL 130
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RESULT 7
ENTRY B57378 #type complete
TITLE cyclin-dependent kinase inhibitor p19 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
20-Sep-1999
ACCESSIONS B57378
REFERENCE Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
#authors Mol. Cell. Biol. (1995) 15:2682-2688
#journal Identification of human and mouse p19, a novel CDK4 and CDK6
#title inhibitor with homology to p16(ink4).
#crosso-references PMID:95257949
#accession B57378
#status preliminary
#molecule_type mRNA
#residues 1-166 #label CHA

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DATE          06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
              13-Aug-1999
ACCESSIONS    S37431; A39643; B39643; A40334; A49462; S14533; S14569
REFERENCE     S37431
#authors      Chan, W.
#submission   submitted to the EMBL Data Library, September 1993
#accession    S37431
#status       preliminary
#molecule_type mRNA
#residues     1-3924 #label CHA
#cross-references EMBL:Z26634; NID:9406287; PIDN:CAA81387.1;
              PID:9406288

REFERENCE     A39643
#authors      Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
#journal      J. Cell Biol. (1991) 114:241-253
#title        Isolation and characterization of cDNAs encoding human brain
              ankyrins reveal a family of alternatively spliced genes.
#cross-references MUID:91302466
#accession    A39643
#status       preliminary
#molecule_type mRNA
#residues     1-1443,3585-3924 #label OTT
#cross-references EMBL:X56958

REFERENCE     A40334
#authors      Tse, W.T.; Meuninger, J.C.; Yang-Feng, T.L.; Francke, U.;
              Sahr, K.E.; Lux, S.E.; Ward, D.C.; Forget, B.G.
#journal      Genomics (1991) 10:858-866
#title        Isolation and chromosomal localization of a novel
              nonerythroid ankyrin gene.
#cross-references MUID:92009921
#accession    A40334
#status       preliminary
#molecule_type DNA
#residues     463-474, 'PE', 477-495 #label TSE
#cross-references GB:M37133; NID:9178647; PIDN:AAA62828.1; PID:9178648

REFERENCE     A49462
#authors      Chan, W.; Kordeli, E.; Bennett, V.
#journal      J. Cell Biol. (1993) 123:1463-1473
#title        440-kD ankyrinB: structure of the major developmentally
              regulated domain and selective localization in unmyelinated
              axons.
#cross-references MUID:94075409
#accession    A49462
#status       preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues     1-3924 #label RES
#cross-references EMBL:Z26634; NID:9406287; PIDN:CAA81387.1;
              PID:9406288

GENETICS
#gene         GDB:ANK2
#map_position 4q25-q27
#classification #superfamily ankyrin; ankyrin repeat homology
#keywords      alternative splicing
#feature       2-3924
              #product ankyrin 2, long form #status predicted #label
              MAV
              #product ankyrin 2, short form #status predicted #label
              MAV

63-95         #domain ankyrin repeat homology #label AN01\
96-128        #domain ankyrin repeat homology #label AN02\
129-161        #domain ankyrin repeat homology #label AN03\
162-190        #domain ankyrin repeat homology #label AN04\
191-223        #domain ankyrin repeat homology #label AN05\
232-264        #domain ankyrin repeat homology #label AN06\
265-297        #domain ankyrin repeat homology #label AN07\
298-330        #domain ankyrin repeat homology #label AN08\
331-363        #domain ankyrin repeat homology #label AN09\
364-396        #domain ankyrin repeat homology #label AN10\

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397-429        #domain ankyrin repeat homology #label AN11\
430-462        #domain ankyrin repeat homology #label AN12\
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496-528        #domain ankyrin repeat homology #label AN14\
529-561        #domain ankyrin repeat homology #label AN15\
562-594        #domain ankyrin repeat homology #label AN16\
595-627        #domain ankyrin repeat homology #label AN17\
628-660        #domain ankyrin repeat homology #label AN18\
661-693        #domain ankyrin repeat homology #label AN19\
694-726        #domain ankyrin repeat homology #label AN20\
727-759        #domain ankyrin repeat homology #label AN21\
760-792        #domain ankyrin repeat homology #label AN22\
793-825        #domain ankyrin repeat homology #label AN23\
SUMMARY       #length 3924 #molecular-weight 430340 #checksum 3664

Query Match   16.8%; Score 181; DB 2; Length 3924;
Best Local Similarity 38.1%; Pred. No. 3.58e-12;
Matches 48; Conservative 20; Mismatches 53; Indels 5; Gaps 4;

Db 471 AARAGQVEVYRCILLRNGALVDAREREQPLHIAASLGKTEIVQLLOHMAHPDAATNG 530
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 20 AAR-GRVEEVRALEVALPNAPNSYGRPIQVM-MGSGARVAELLLHGAEPNCADPAT 77
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 531 YT-PLHISAREGOVDVAVSLLEAGAAHSLATKKGFTPLHVAAYGSLDVAKLLQRRAAA 589
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 78 LTRPVHDAREGEFLDTLVLRHAGARLDVDRDANGRLPVDLAELGHRDVARYL--RAAAG 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 590 DSAGKN 595
      : |||
QY 136 GTRGSN 141

RESULT 12
ENTRY   B35049
TITLE   ankyrin 1, erythrocyte splice form 3 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS   ankyrin 2.2, erythrocyte
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change
              10-Jul-1998

ACCESSIONS B35049
REFERENCE   B35049
#authors   Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.;
              Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.;
              Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734.
#title     cDNA sequence for human erythrocyte ankyrin.
#cross-references MUID:90175370
#accession B35049
#status     preliminary
#molecule_type mRNA
#residues   1-1856 #label LAM

GENETICS
#gene       GDB:ANK1; ANK
#map_position 8p11.2-8p11.2
#classification #superfamily ankyrin; ankyrin repeat homology
#keywords      alternative splicing
#feature       2-1856
              #product ankyrin 1, erythrocyte form 3 #status predicted
              #label MAV
              #product ankyrin 2.2, erythrocyte #status predicted
              #label MA2\

44-76         #domain ankyrin repeat homology #label AN01\
77-109        #domain ankyrin repeat homology #label AN02\
110-142       #domain ankyrin repeat homology #label AN03\
143-171       #domain ankyrin repeat homology #label AN04\
172-204       #domain ankyrin repeat homology #label AN05\
205-237       #domain ankyrin repeat homology #label AN06\
238-270       #domain ankyrin repeat homology #label AN07\
271-303       #domain ankyrin repeat homology #label AN08\
304-336       #domain ankyrin repeat homology #label AN09\
337-369       #domain ankyrin repeat homology #label AN10\
370-402       #domain ankyrin repeat homology #label AN11\

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403-435 #domain ankyrin repeat homology #label AN12\
436-468 #domain ankyrin repeat homology #label AN13\
469-501 #domain ankyrin repeat homology #label AN14\
502-534 #domain ankyrin repeat homology #label AN15\
535-567 #domain ankyrin repeat homology #label AN16\
568-600 #domain ankyrin repeat homology #label AN17\
601-633 #domain ankyrin repeat homology #label AN18\
634-666 #domain ankyrin repeat homology #label AN19\
667-699 #domain ankyrin repeat homology #label AN20\
700-732 #domain ankyrin repeat homology #label AN21\
733-765 #domain ankyrin repeat homology #label AN22\
766-798 #domain ankyrin repeat homology #label AN23\
SUMMARY #length 1856 #molecular-weight 203445 #checksum 6521

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Matches 46; Conservative 16; Mismatches 50; Indels 6; Gaps 6;

Db 507 LHIAAREGHVETVLLALEKEASQACMTKGGFTPLHVAAYKGVKRVVAELLERDAHPNAAG 566
QY 16 LATAAARGVEEVRALLEVALPNAPNSYGRRIQVMM-GSARVAELLHLHGAEPNCAD 74

Db 567 KNGLT-PLHVAHHNNLDIVKLLPRGGSP-HSP-ANNGYTPLHIAAKQNOVEVARSL 621
QY 75 PATLTPVHDAAREGFLDTL-VVLHAGARLDVDRDAW-GRLPVDLAEELGHEDVARYL 130

RESULT 13
ENTRY SJHUK #type complete
TITLE ankyrin 1, erythrocyte splice form 2 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS ankyrin 2.2
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change
04-Sep-1998

ACCESSIONS A35049
REFERENCE #authors Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.;
Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
#title cDNA sequence for human erythrocyte ankyrin.
#cross-references MUID:90175370
#accession A35049
#status preliminary
#molecule_type mRNA
#residues 1-1880 #label LAM
#cross-references GB:M28880

GENETICS
#gene GDB:ANK1; ANK
#cross-references GDB:118737; OMIM:182900
#map_position 9p11.2-9p11.2
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS alternative splicing; cytoskeleton
FEATURE
2-1880 #product ankyrin 1, erythrocyte form 2 #status predicted
#label MA1\
#label MA2\
2-1513,1676-1880 #product ankyrin 2.2, erythrocyte #status predicted
#label AN1\
#label AN2\
#domain ankyrin repeat homology #label AN01\
#domain ankyrin repeat homology #label AN02\
#domain ankyrin repeat homology #label AN03\
#domain ankyrin repeat homology #label AN04\
#domain ankyrin repeat homology #label AN05\
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#domain ankyrin repeat homology #label AN07\
#domain ankyrin repeat homology #label AN08\
#domain ankyrin repeat homology #label AN09\
#domain ankyrin repeat homology #label AN10\
#domain ankyrin repeat homology #label AN11\
#domain ankyrin repeat homology #label AN12\
#domain ankyrin repeat homology #label AN13\
#domain ankyrin repeat homology #label AN14\
#domain ankyrin repeat homology #label AN15\

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535-567 #domain ankyrin repeat homology #label AN16\
568-600 #domain ankyrin repeat homology #label AN17\
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634-666 #domain ankyrin repeat homology #label AN19\
667-699 #domain ankyrin repeat homology #label AN20\
700-732 #domain ankyrin repeat homology #label AN21\
733-765 #domain ankyrin repeat homology #label AN22\
766-798 #domain ankyrin repeat homology #label AN23\
SUMMARY #length 1880 #molecular-weight 206066 #checksum 6968

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Best Local Similarity 39.0%; Pred. No. 4.30e-11;
Matches 46; Conservative 16; Mismatches 50; Indels 6; Gaps 6;

Db 507 LHIAAREGHVETVLLALEKEASQACMTKGGFTPLHVAAYKGVKRVVAELLERDAHPNAAG 566
QY 16 LATAAARGVEEVRALLEVALPNAPNSYGRRIQVMM-GSARVAELLHLHGAEPNCAD 74

Db 567 KNGLT-PLHVAHHNNLDIVKLLPRGGSP-HSP-ANNGYTPLHIAAKQNOVEVARSL 621
QY 75 PATLTPVHDAAREGFLDTL-VVLHAGARLDVDRDAW-GRLPVDLAEELGHEDVARYL 130

RESULT 14
ENTRY SJHUK #type complete
TITLE ankyrin 1, erythrocyte splice form 1 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS ankyrin 2.2
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
22-Jun-1999

ACCESSIONS S08275; A33219; PC2220; A35443
REFERENCE #authors Lux, S.E.; John, K.M.; Bennett, V.
#journal Nature (1990) 344:36-42
#title Analysis of cDNA for human erythrocyte ankyrin indicates a
repeated structure with homology to tissue-differentiation
and cell-cycle control proteins.
#cross-references MUID:90158830
#accession S08275
#molecule_type mRNA
#residues 1-1881 #label LUL
#cross-references EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702
#accession A33219
#molecule_type protein
#residues 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30; 733-749, 'A', 751-753;
828-833, 'X', 835-855, 'X', 857-859, 'XX', 862-871; 959-1003;
1106-1120, 'XX', 1123-1128; 1149-1172; 1282-1285, 'E',
1287-1288; 1307-1332; 1345-1365, 'X', 1367; 1383-1427;
1601-1630; 1686-1698, 'D', 1700; 1763-1772 #label LUX
#note 845-Arg and 1392-thr were also found
PC2220
#authors Hermann, J.; Barel, M.; Frade, R.
#journal Biochem. Biophys. Res. Commun. (1994) 204:453-460
#title Human erythrocyte ankyrin, a cytoskeleton component,
generates the p57 membrane proteinase which cleaves C3, the
third component of complement.
#cross-references MUID:95071348
#accession PC2220
#molecule_type protein
#residues 910-929 #label HER
REFERENCE A35443
#authors Davis, L.H.; Bennett, V.
#journal J. Biol. Chem. (1990) 265:10589-10596
#title Mapping the binding sites of human erythrocyte ankyrin for
the anion exchanger and spectrin.
#cross-references MUID:90285190
#accession A35443
#molecule_type protein
#residues 'X', 5, 'X', 7-12; 403-417, 'X', 419-422, 'H', 424, 'IQ', 797-800,
'L', 802-814; 862-863, 'X', 865-877; 'X', 899-901, 'T',
903-909, 'X', 911-912 #label DAV

GENETICS

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#gene GDB:ANK1: ANK
##cross-references GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS alternative splicing; phosphoprotein
FEATURE
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#product ankyrin 1, erythrocyte form 1 #status predicted
#label MAT1\
#label MAT2\
2-1512,1675-1881
#product ankyrin 2.2, erythrocyte #status predicted
#label MAT2\
#domain 89K #status predicted #label DOM1\
#region anion exchange protein binding\
#domain ankyrin repeat homology #label ANO1\
#domain ankyrin repeat homology #label ANO2\
#domain ankyrin repeat homology #label ANO3\
#domain ankyrin repeat homology #label ANO4\
#domain ankyrin repeat homology #label ANO5\
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#domain ankyrin repeat homology #label ANO22\
#domain ankyrin repeat homology #label ANO23\
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#region spectrin binding\
#domain 55K #status predicted #label DOM3
#length 1881 #molecular-weight 206275 #checksum 2619
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Matches 46; Conservative 16; Mismatches 50; Indels 6; Gaps 6;
Db 507 LHIAAREGHVYVYLALEKEASQACMTKGGFTPLHVAARYKVRVLAELLEDHAPNAAG 566
QY 16 LATAARGVEEVRALEVALPNAPNSYGRPIQVMM-GSARVAELLLHGAEPNCAD 74
Db 567 KNGLT-PLHAVHNNLDIVKLLPRGGSP-HSP-ANWGYTTPHIAKONQVEVARSL 621
QY 75 PATLTRPVHDAAREGFDTL-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARYL 130
ends are found among transcripts of the erythroid ankyrin gene.
#cross-references MUID:93252825
#accession S3771
#status preliminary
#molecule_type mRNA
#residues 1-1848 #label BIR
##cross-references EMBL:X69063; NID:g311816; PIDN:CAA48801.1;
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PID:g311817
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS alternative splicing
FEATURE
48-80
81-113
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147-175
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209-241
242-274
275-307
308-340
341-373
374-406
407-439
440-472
473-505
506-538
539-571
572-604
605-637
638-670
671-703
704-736
737-769
770-802
SUMMARY
#length 1848 #molecular-weight 202576 #checksum 2542
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Best Local Similarity 38.1%; Pred. No. 6.11e-11;
Matches 45; Conservative 17; Mismatches 50; Indels 6; Gaps 6;
Db 511 LHIAAREGHVYVYLALEKEASQACMTKGGFTPLHVAARYKVRVLAELLEDHAPNAAG 570
QY 16 LATAARGVEEVRALEVALPNAPNSYGRPIQVMM-GSARVAELLLHGAEPNCAD 74
Db 571 KNGLT-PLHAVHNNLDIVKLLPRGGSP-HSP-ANWGYTTPHIAKONQVEVARSL 625
QY 75 PATLTRPVHDAAREGFDTL-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARYL 130
Search completed: Thu Jul 20 08:35:26 2000
Job time : 14 secs.
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MPSRH

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:35:43 2000; MasPar time 7.46 Seconds
637.235 Million cell updates/sec

Tabular output not generated.

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pap
Perfect Score: 1078
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAEGPSDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 44.859; Variance 85.215; scale 0.526

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
Result No.	Score	Query Match	Description	ID	Pred. No.
1	1067	99.0	CYCLIN-DEPENDENT KINASE	CDN2_HUMAN	1.98e-199
2	729	67.6	CYCLIN-DEPENDENT KINASE	CDN5_MOUSE	6.89e-126
3	725	67.3	CYCLIN-DEPENDENT KINASE	CDN5_HUMAN	5.00e-125
4	720	66.8	CYCLIN-DEPENDENT KINASE	CDN5_RAT	5.94e-124
5	663	61.5	CYCLIN-DEPENDENT KINASE	CDN2_MOUSE	9.94e-112
6	575	53.3	CYCLIN-DEPENDENT KINASE	CDN2_MONDO	5.27e-93
7	364	33.8	CYCLIN-DEPENDENT KINASE	CDN7_HUMAN	3.10e-49
8	341	31.6	CYCLIN-DEPENDENT KINASE	CDN7_MOUSE	1.29e-44
9	300	27.8	CYCLIN-DEPENDENT KINASE	CDN6_HUMAN	1.72e-36
10	292	27.1	CYCLIN-DEPENDENT KINASE	CDN6_MOUSE	6.33e-35
11	181	16.8	ANKYRIN, BRAIN VARIANT	ANKC_HUMAN	3.37e-14
12	181	16.8	ANKYRIN, BRAIN VARIANT	ANKB_HUMAN	3.37e-14
13	174	16.1	ANKYRIN, BRAIN VARIANT	ANKI_MOUSE	5.58e-13
14	173	16.0	ANKYRIN, BRAIN VARIANT	ANKI_HUMAN	8.30e-13
15	143	13.3	NEUROGENIC LOCUS NOTCH	NTC4_MOUSE	8.65e-08
16	141	13.1	DEATH-ASSOCIATED PROTEIN	DAPK_HUMAN	1.81e-07
17	136	12.6	ANKYRIN HOMOLOG PRECURSOR	ANKH_CHRV1	1.13e-06
18	128	11.9	NEUROGENIC LOCUS NOTCH	NTC3_MOUSE	1.99e-05
19	126	11.7	NEUROGENIC LOCUS NOTCH	NTC3_DROME	4.03e-05
20	124	11.5	NEUROGENIC LOCUS NOTCH	NTC1_RAT	8.10e-05
21	123	11.4	NEUROGENIC LOCUS NOTCH	NTC1_BRARE	1.15e-04
22	123	11.4	NEUROGENIC LOCUS NOTCH	NTC1_HUMAN	1.15e-04
23	123	11.4	NEUROGENIC LOCUS NOTCH	NOTC_XENLA	1.15e-04

ALIGNMENTS				Pred. No.	
Result No.	Score	Query Match	Description	ID	Pred. No.
24	122	11.3	GA BINDING PROTEIN	GABD_MOUSE	1.62e-04
25	119	11.0	POTASSIUM-DEPENDENT RIBONUCLEASE	GLS1_CAEEL	4.54e-04
26	119	11.0	NEUROGENIC LOCUS NOTCH	NTS1_MOUSE	4.54e-04
27	119	11.0	NEUROGENIC LOCUS NOTCH	NTS1_MOUSE	4.54e-04
28	117	10.9	PHLB PROTEIN PRECURSOR	PHLB_SERLI	6.37e-04
29	118	10.9	GA BINDING PROTEIN	GABC_MOUSE	6.37e-04
30	118	10.9	GA BINDING PROTEIN	GABB_MOUSE	6.37e-04
31	117	10.9	SKD3 PROTEIN	SKD3_MOUSE	8.94e-04
32	115	10.7	GA BINDING PROTEIN	GABD_HUMAN	1.75e-03
33	115	10.7	GA BINDING PROTEIN	GABB_HUMAN	1.75e-03
34	114	10.6	ALPHA-LATROTOXIN PRECURSOR	LATA_LATMA	2.45e-03
35	111	10.3	TRANSCRIPTIONAL ACTIVATOR	FNRL_RHOSH	6.59e-03
36	109	10.1	HYPOTHETICAL 24.0 KD P	Y282_MYCTU	1.27e-02
37	108	10.0	HYPOTHETICAL BANHI-ORF	YB13_FOPDM	1.75e-02
38	108	10.0	HYPOTHETICAL 20.8 KD P	YOAB_ECOLI	1.75e-02
39	108	10.0	HYPOTHETICAL 48.5 KD P	YE07_MYCTU	1.75e-02
40	105	9.7	HYPOTHETICAL 123.6 KD P	YIL2_YEAST	4.57e-02
41	104	9.6	B-CELL LYMPHOMA 3-ENCO	BCL3_HUMAN	6.26e-02
42	101	9.4	ENDOGLIN PRECURSOR	EGLN_MOUSE	1.60e-01
43	100	9.3	PROTEIN UL17	UL17_HSV11	2.17e-01
44	100	9.3	HYPOTHETICAL PROTEIN K	Y050_HUMAN	2.17e-01
45	100	9.3	OXYGEN-REGULATED PROTEIN	ORP1_HUMAN	2.17e-01

Cancer Surv. 26:115-132(1996).

[6] REVIEW ON VARIANTS.

RA MEDLINE; 96303699.

RA Smith-Soerensen B., Kovig E.;

RT "CDKN2A (p16INK4a) somatic and germline mutations.";

RL Hum. Mutat. 7:294-303(1996).

[7] VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).

RA MEDLINE; 94338359.

RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;

RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41

RT (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small

RT cell lung carcinomas.";

RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).

[8] VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.

RA MEDLINE; 95078916.

RA Hussusian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T., N.C.;

RA Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;

RT "Germline p16 mutations in familial melanoma.";

RL Nat. Genet. 8:15-21(1994).

[9] VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.

RA MEDLINE; 95060835.

RA Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,

RA Abraham J.M., Meltzer S.J.;

RT "The MTS1 gene is frequently mutated in primary human esophageal

RT tumors.";

RL Oncogene 9:3737-3741(1994).

[10] VARIANTS.

RA MEDLINE; 95188190.

RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,

RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,

RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;

RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in

RT primary and metastatic lung cancer.";

RL Cancer Res. 55:1448-1451(1995).

[11] VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.

RA MEDLINE; 96121580.

RA Walker G.J., Hussusian C.J., Flores J.F., Glendening J.M.,

RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;

RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma

RT kindreds.";

RL Hum. Mol. Genet. 4:1845-1852(1995).

[12] CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.

RA MEDLINE; 95375774.

RA Ranade K., Hussusian C.J., Sikorski R.S., Varmus H.E.,

RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,

RA Dracopoli N.C.;

RT "Mutations associated with familial melanoma impair p16INK4

RT function.";

RL Nat. Genet. 10:114-116(1995).

[13] VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.

RA MEDLINE; 96323259.

RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,

RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,

RA Isseilbacher K.J., Sober A.J., Haber D.A.;

RT "Prevalence of germline mutations in p16, p19ARF, and CDK4 in

RT familial melanoma: analysis of a clinic-based population.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).

[14] VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.

RA MEDLINE; 97472457.

RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,

RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,

RA Bishop D.T., Bishop J.N.;

RT "Germline mutations of the CDKN2 gene in UK melanoma families.";

RL Hum. Mol. Genet. 6:2061-2067(1997).

[15] VARIANTS FAMILIAL MELANOMA.

RP MEDLINE; 98087572.

RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,

RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;

RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone

RT families in France.";

RL Hum. Mol. Genet. 7:209-216(1998).

[16] ERRATUM.

RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,

RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;

RL Hum. Mol. Genet. 7:941-941(1998).

[17] VARIANT PANCREATIC CARCINOMA CYS-146.

RA Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,

RA Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;

RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple

RT pancreatic carcinomas.";

RL Hum. Mutat. 12:70-70(1998).

[18] VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.

RA Gretarsdottir S., Olafsdottir G.H., Borg A.;

RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,

RT glioma and carcinoma of the pancreas.";

RL Hum. Mutat. 12:212-212(1998).

CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS

CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE

CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.

CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.

CC -1- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A

CC WIDE RANGE OF TISSUES.

CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE

CC INHIBITORS.

CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.

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EMBL; L27211; RAA92554.1; -

EMBL; U12820; RAB60645.1; -

EMBL; U12818; RAB60645.1; JOINED.

EMBL; U12819; RAB60645.1; JOINED.

EMBL; S69804; RAD14048.1; -

PDB; 1BI7; 16-FEB-99.

MIM; 600160; -

PFAM; PF00023; ank; 3.

Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;

Polymorphism; 3D-structure.

DOMAIN 12 141

REPEAT 12 43

REPEAT 44 75

REPEAT 77 109

REPEAT 110 141

VARIANT 14 14

VARIANT 16 16

FTID-Var_001408.

L -> P (IN A BILIARY TRACT TUMOR AND A

FAMILIAL MELANOMA).

FTid=VAR_001409.

A -> P (IN A LUNG TUMOR AND MELANOMA).

FTid=VAR_001410.

A -> S (IN A BILIARY TRACT TUMOR).

FTid=VAR_001411.

G -> D (IN A PANCREAS TUMOR).

FTid=VAR_001412.

R -> C (IN MELANOMA).

FTid=VAR_001413.

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FT VARIANT 24 24 R -> P (IN FAMILIAL MELANOMA AND
FT MELANOMA).
FT /FTID=VAR_001414.
FT E -> D (IN A BILIARY TRACT TUMOR).
FT /FTID=VAR_001415.
FT L -> P (IN FAMILIAL MELANOMA).
FT /FTID=VAR_001416.
FT E -> D (IN A BILIARY TRACT TUMOR).
...
Note: remainder of annotations omitted.

Query Match 99.0%; Score 1067; DB 1; Length 156;
Best Local Similarity 98.7%; Pred. No. 1.98e-199;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MEPAAGSMPEPSADWLATAAARGVEEVRLLEAGALPNAPNSYGRRPPIQVMMGMSARVA 60
QY 1 MDPAGSMPEPSADWLATAAARGVEEVRLLEAGALPNAPNSYGRRPPIQVMMGMSARVA 60
Db 61 ELLLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAE 120
QY 61 ELLLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAE 120
Db 121 LGRDVARYLRAAAGTRGSNHRIDAAREGSPDIP 156
QY 121 LGRDVARYLRAAAGTRGSNHRIDAAREGSPDIP 156

RESULT 2
ID CDN5_MOUSE STANDARD; PRT; 130 AA.
AC P55271.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
RX MEDLINE; 95380169.
RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RA "Cloning and characterization of murine p16INK4a and p15INK4b genes."
RA Oncogene 11:635-645(1995).
[2]
SEQUENCE FROM N.A.
RX STRAIN-C57BL/6J X DBA;
RX MEDLINE; 9732242.
RA Malumbres M., de Castro I., Santos J., Melendez B., Manges R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RT "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by
RT deletion and de novo methylation with independence of p16INK4a
RT alterations in murine primary T-cell lymphomas."
RT Oncogene 14:1361-1370(1997).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -1- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED UBQUITOUSLY.
CC -1- INDUCTION: BY TGF-BETA.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
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CC or send an email to license@isb-sib.ch).
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CC -----
DR EMBL; U66085; AAB39833.1;
DR EMBL; U66084; AAB39833.1; JOINED.
DR MGD; MG1:104737; CDKN2B.
DR PFAM; PF00023; ank; 3.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.
FT DOMAIN 5 95 2 X ANK MOTIF REPEATS.
FT REPEAT 5 31 ANK MOTIF 1 (INCOMPLETE).
FT REPEAT 65 95 ANK MOTIF 2.
SQ SEQUENCE 130 AA; 13788 MW; 7AAD60FF552BCFF9 CRC64;

Query Match 67.6%; Score 729; DB 1; Length 130;
Best Local Similarity 88.3%; Pred. No. 6.89e-126;
Matches 106; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 10 LATAAARGVETRYQLLEAGALPNALNFRGRRPIQVMMGMSAQVAELLLHGAENPCADP 69
QY 16 LATAAARGVEEVRLLEAGALPNAPNSYGRRPPIQVMMGMSARVAELLLHGAENPCADP 75
Db 70 ATLTPRVHDAAREGFLDTLVVLRAGARLDVCDAGRLPVDLAEEOGHRIARYLHAATG 129
QY 76 ATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAEELGHRDVARYLRAAG 135

RESULT 3
ID CDN5_HUMAN STANDARD; PRT; 138 AA.
AC P42772.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
DE (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).
GN CDKN2B OR MTS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
[1]
SEQUENCE FROM N.A.
RX MEDLINE; 95095079.
RA Guan K.-L., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
RA Matera G.A., Xiong Y.;
RT "Growth suppression by p18, a p16INK4a/MTS1- and p14INK4b/MTS2-related
RT CDK6 inhibitor, correlates with wild-type pRb function."
RL Genes Dev. 8:2939-2952(1994).
[2]
SEQUENCE FROM N.A.
RX MEDLINE; 94359613.
RA Hannon G.J., Beach D.;
RT "p15INK4b is a potential effector of TGF-beta-induced cell cycle
RT arrest."
RL Nature 371:257-261(1994).
[3]
SEQUENCE OF 53-138 FROM N.A.
RX MEDLINE; 94204645.
RA Kamb A., Gius N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
RA Skolnick M.H.;
RT "A cell cycle regulator potentially involved in genesis of many tumor
RT types."
RL Science 264:436-440(1994).
[4]
VARIANTS LUNG ADENOCARCINOMA GLO-47 AND VAL-50.
RX MEDLINE; 95188190.
RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,
RA Xiong Y., Beach D.H., Yokota J., Harris C.C.;
RT "Mutations in the p16INK4a/MTS1/CDKN2, p15INK4b/MTS2, and p18 genes in
RT primary and metastatic lung cancer."
RL Cancer Res. 55:1448-1451(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -1- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -1- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
```


Db 63 PNLDKGTGFA-VIHDAARAGFLDTQALLERQADVNIEDNEGNPLHLAAKEGLHPVVEF 121
 Qy 70 PNCADPATLRPVHDAAREGEFLDTLVVLRAGARLDVRDANGRLPVDLAELGHRDVARY 129

Db 122 L 122
 Qy 130 L 130

RESULT 11
 ID ANKC_HUMAN STANDARD; PRT; 1839 AA.
 AC Q01485;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)
 DE (FRAGMENT).
 GN ANK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN STEM;
 RX MEDLINE; 91302466.
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and characterization of cDNAs encoding human brain
 RT ankyrins reveal a family of alternatively spliced genes.";
 RT J. Cell Biol. 114:241-253(1991).
 [2]
 RP SEQUENCE OF 463-495 FROM N.A.
 RX MEDLINE; 92009921.
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and chromosomal localization of a novel nonerythroid
 RT ankyrin gene.";
 RT Genomics 10:858-866(1991).
 CC -1- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
 CC SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
 CC BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85,
 CC AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
 CC DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO
 CC THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -1- ALTERNATIVE PRODUCTS: THE TWO BRAIN VARIANTS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF GENE ANK2.
 CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
 CC CELLS THROUGHOUT THE BRAIN.
 CC -1- SIMILARITY: CONTAINS 24 ANK REPEATS.

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 DR EMBL; X56958; G29491; .
 DR EMBL; M37123; AAA62828.1; .
 DR PIR; S14569; S14569.
 DR PIR; B39643; B39643.
 DR HSP; Q00420; IAWC.
 DR MIM; 106410; .
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PFAM; PF00023; ank; 22.
 DR PFAM; PF00531; death; 1.
 DR PFAM; PF00791; ZU5; 1.
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Multigene family. 63 792 22 X ANK MOTIF REPEATS.
 FT DOMAIN 63 95 ANK MOTIF 1.
 FT REPEAT 96 128 ANK MOTIF 2.
 FT REPEAT

FT REPEAT 129 161 ANK MOTIF 3.
 FT REPEAT 162 190 ANK MOTIF 4.
 FT REPEAT 191 231 ANK MOTIF 5.
 FT REPEAT 232 264 ANK MOTIF 6.
 FT REPEAT 265 297 ANK MOTIF 7.
 FT REPEAT 298 330 ANK MOTIF 8.
 FT REPEAT 331 363 ANK MOTIF 9.
 FT REPEAT 364 396 ANK MOTIF 10.
 FT REPEAT 397 429 ANK MOTIF 11.
 FT REPEAT 430 462 ANK MOTIF 12.
 FT REPEAT 463 495 ANK MOTIF 13.
 FT REPEAT 496 528 ANK MOTIF 14.
 FT REPEAT 529 561 ANK MOTIF 15.
 FT REPEAT 562 594 ANK MOTIF 16.
 FT REPEAT 595 627 ANK MOTIF 17.
 FT REPEAT 628 660 ANK MOTIF 18.
 FT REPEAT 661 693 ANK MOTIF 19.
 FT REPEAT 694 726 ANK MOTIF 20.
 FT REPEAT 727 759 ANK MOTIF 21.
 FT REPEAT 760 792 ANK MOTIF 22.
 FT DOMAIN 1451 1535 DEATH DOMAIN.
 FT CONFLICT 475 476
 FT NON_TER 1839 1839 GQ -> PE (IN REF. 2).
 SQ SEQUENCE 1839 AA; 202409 MW; 5C1C1FD3D795A280 CRC64;

Query Match 16.8%; Score 181; DB 1; Length 1839;
 Best Local Similarity 38.1%; Pred. No. 3.37e-14;
 Matches 48; Conservative 20; Mismatches 53; Indels 5; Gaps 4;

Db 471 AARAGOVVVRCLLRNGALVDARAREQOTPLHIASRLGKTEIVOLLQHMHPDAATTNG 530
 Qy 20 AAR-GRVEEVRALEVALPNAPNSYGRPIQVW-MGSAARVAELLHLGAEPCADPAT 77
 Db 531 YT-PLHISAREQVDVASVLEAGAAHSLATKKGFTPLHVAAKYGSGLDVAKLLQRRAAA 589
 Qy 78 LTRPVHDAAREGEFLDTLVVLRAGARLDVRDANGRLPVDLAELGHRDVARYL--RAAAG 135
 Db 590 DSAGKN 595
 Qy 136 GTRGSN 141

RESULT 12
 ID ANKB_HUMAN STANDARD; PRT; 3924 AA.
 AC Q01484; 1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).
 GN ANK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN STEM;
 RX MEDLINE; 94075409.
 RA Chan W., Kordell E., Bennett V.;
 RA "440-KD ankyrinB: structure of the major developmentally regulated
 RA domain and selective localization in unmyelinated axons.";
 RL J. Cell Biol. 123:1463-1473(1993).
 [2]
 RP SEQUENCE OF 1-2077 FROM N.A.
 RC TISSUE-BRAIN STEM;
 RX MEDLINE; 91302466.
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
 RA "Isolation and characterization of cDNAs encoding human brain
 RA ankyrins reveal a family of alternatively spliced genes.";
 RL J. Cell Biol. 114:241-253(1991).
 CC -1- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
 CC SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
 CC BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85,
 CC AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND

CC DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO
 CC THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -1- ALTERNATIVE PRODUCTS: THE TWO BRAIN VARIANTS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF GENE ANK2.
 CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
 CC CELLS THROUGHOUT THE BRAIN.
 CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
 CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
 CC AND FUNCTION (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 24 ANK REPEATS.
 CC -----
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 CC -----
 CC EMBL; Z26634; CAA81387.1; -;
 CC DR EMBL; X56957; CAA40278.1; -;
 CC DR PIR; S14533; S14533.
 CC DR PIR; A39643; A39643.
 CC DR HSP; Q00420; IAWC.
 CC DR MM; 106410; -;
 CC DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
 CC DR PFAM; PF00023; ank; 22.
 CC DR PFAM; PF00531; death; 1.
 CC DR PFAM; PF00791; ZU5; 1.
 CC KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 CC KW Phosphorylation; Multigene family.
 CC FT DOMAIN 63 792 24 X ANK MOTIF REPEATS.
 CC FT REPEAT 63 95 ANK MOTIF 1.
 CC FT REPEAT 96 128 ANK MOTIF 2.
 CC FT REPEAT 129 161 ANK MOTIF 3.
 CC FT REPEAT 162 190 ANK MOTIF 4.
 CC FT REPEAT 191 231 ANK MOTIF 5.
 CC FT REPEAT 232 264 ANK MOTIF 6.
 CC FT REPEAT 265 297 ANK MOTIF 7.
 CC FT REPEAT 298 330 ANK MOTIF 8.
 CC FT REPEAT 331 363 ANK MOTIF 9.
 CC FT REPEAT 364 396 ANK MOTIF 10.
 CC FT REPEAT 397 429 ANK MOTIF 11.
 CC FT REPEAT 430 462 ANK MOTIF 12.
 CC FT REPEAT 463 495 ANK MOTIF 13.
 CC FT REPEAT 496 528 ANK MOTIF 14.
 CC FT REPEAT 529 561 ANK MOTIF 15.
 CC FT REPEAT 562 594 ANK MOTIF 16.
 CC FT REPEAT 595 627 ANK MOTIF 17.
 CC FT REPEAT 628 660 ANK MOTIF 18.
 CC FT REPEAT 661 693 ANK MOTIF 19.
 CC FT REPEAT 694 726 ANK MOTIF 20.
 CC FT REPEAT 727 759 ANK MOTIF 21.
 CC FT REPEAT 760 792 ANK MOTIF 22.
 CC FT DOMAIN 1773 1950 REPEAT-RICH REGION.
 CC FT REPEAT 1773 1784 REPEAT A.
 CC FT REPEAT 1785 1796 REPEAT A.
 CC FT REPEAT 1797 1808 REPEAT A.
 CC FT REPEAT 1809 1820 REPEAT A.
 CC FT REPEAT 1821 1832 REPEAT A.
 CC FT REPEAT 1833 1844 REPEAT A.
 CC FT REPEAT 1845 1856 REPEAT A.
 CC FT REPEAT 1857 1867 REPEAT A.
 CC FT REPEAT 1868 1879 REPEAT A.
 CC FT REPEAT 1880 1891 REPEAT A.
 CC FT REPEAT 1892 1902 REPEAT A.
 CC FT REPEAT 1903 1914 REPEAT A.
 CC FT REPEAT 1915 1926 REPEAT A.
 CC FT REPEAT 1927 1938 REPEAT A.
 CC FT REPEAT 1939 1950 REPEAT A.
 CC FT DOMAIN 3536 3620 DEATH DOMAIN.
 CC FT SEQUENCE 3924 AA; 430337 MW; 52AC496C428E29D2 CRC64;

Query Match 16.68; Score 181; DB 1; Length 3924;
 Best Local Similarity 38.1%; Pred. No. 3.37e-14;
 Matches 48; Conservative 20; Mismatches 53; Indels 5; Gaps 4;
 Db 471 AARAGOVVEVRCLLRNGALVDARAREBOTPLHIAIRSLRGKTEIVOLLQHMHPDAATNG 530
 QY 20 AAR-GRVEFVRLLEVALPNAPNSYGRRIQVW-MGSRARVAELLLHGAEPNCADPAT 77
 Db 531 YT-PLHISAREGOVDVASVLLERAGAAHSLATKKGFTPLHVAARYGSLDVAKLLQRAAA 589
 QY 78 LTRPVHDAAREGEFLDTLVLLHRAAGARDVDRDAMGRLPVDLAELGHRDVARYL--RAAAG 135
 Db 590 DSAGKN 595
 QY 136 GTRGSN 141
 RESULT 13
 ID ANK1_HUMAN STANDARD; PRT; 1880 AA.
 AC P16157;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).
 GN ANK1 OR ANK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
 RC TISSUE-HEMATOPOIETIC;
 RX MEDLINE; 90158830.
 RA Lux S.E., John K.M., Bennett V.;
 RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
 RT structure with homology to tissue-differentiation and cell-cycle
 RT control proteins".
 RL Nature 344:36-42(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90175370.
 RA Lambert S., Yu H., Pichal J.T., Lawler J., Ruff P., Speicher D.,
 RA Cheung M.C., Kan Y.W., Palek J.;
 RT "cDNA sequence for human erythrocyte ankyrin".
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
 RN [3]
 RP VARIANT HS ILE-462.
 RX MEDLINE; 96225450.
 RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
 RA Dornwell M., Herbers J., Kugler W., Ozcan R., Pekrun A.,
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive
 RT hereditary spherocytosis".
 RL Nat. Genet. 13:214-218(1996).
 CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
 CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
 CC NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP95, AND TO THE
 CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
 CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
 CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
 CC PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY
 CC ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
 CC VARIANT 2.1.
 CC -1- PTM: REGULATED BY PHOSPHORYLATION.
 CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
 CC -1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE
 CC HEREDITARY SPHEROCYTOSIS (HS).
 CC -1- SIMILARITY: CONTAINS 24 ANK REPEATS.
 CC -----
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or send an email to license@isb-sib.ch).

CC EMBL; X16609; CAA34610.1; -;
DR EMBL; M28880; AAA51732.1; -;
DR PIR; S08275; SJHUK.
DR PIR; A35049; A35049.
DR HSSP; Q00420; IAWC.
DR MIM; 182900; -;
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PFAM; PF00023; ank; 22.
DR PFAM; PF00531; death; 1.
DR PFAM; PF00791; ZU5; 1.
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW Phosphorylation; Lipoprotein; Multigene family; Disease mutation;
KW Elliptocytosis; Polymorphism.
FT INIT_MET 0
FT DOMAIN 1 826 89 KD DOMAIN (ANION EXCHANGE PROTEIN
FT BINDING DOMAIN).
FT DOMAIN 827 1381 62 KD DOMAIN (SPECTRIN BINDING
FT DOMAIN).
FT DOMAIN 1382 1880 55 KD REGULATORY DOMAIN (REGULATES
FT THE BINDING OF ANKYRIN TO SPECTRIN
FT AND THE BAND 3 PROTEIN).
FT 24 X ANK MOTIF REPEATS.
FT ANK MOTIF (INCOMPLETE).
FT 31 777
FT REPEAT 31 42
FT REPEAT 43 75
FT REPEAT 76 108
FT REPEAT 109 141
FT REPEAT 142 170
FT REPEAT 171 203
FT REPEAT 204 236
FT REPEAT 237 269
FT REPEAT 270 302
FT REPEAT 303 335
FT REPEAT 336 368
FT REPEAT 369 401
FT REPEAT 402 434
FT REPEAT 435 467
FT REPEAT 468 500
FT REPEAT 501 533
FT REPEAT 534 566
FT REPEAT 567 599
FT REPEAT 600 632
FT REPEAT 633 665
FT REPEAT 666 698
FT REPEAT 699 731
FT REPEAT 732 764
FT REPEAT 765 777
FT DOMAIN 1402 1486 ANK MOTIF (INCOMPLETE).
FT MISSING (IN ISOFORM 2.2).
FT H -> D (IN ISOFORM 2.2).
FT TVEGLEDPSLEVDIDFMKSHDHTSNP -> ELRGS
FT GLQPLIEGRGAQIVKRAKLKRGKQ (IN A THIRD
FT ISOFORM).
FT R -> T.
FT /FTID-VAR_000595.
FT V -> I (IN HS).
FT /FTID-VAR_000596.
FT R -> H (IN BRUEGGEN).
FT /FTID-VAR_000597.
FT V -> A.
FT /FTID-VAR_000598.
FT D -> E.
FT /FTID-VAR_000599.
FT S -> T.
FT /FTID-VAR_000600.
FT E -> D.
FT /FTID-VAR_000601.

FT VARIANT 1591 1591 D -> N (IN DUESSELDORF).
FT /FTID-VAR_000602.
FT R -> D.
FT VARIANT 1698 1698 /FTID-VAR_000603.
FT CONFLICT 229 229 A -> S (IN REF. 2).
FT CONFLICT 1545 1545 V -> I (IN REF. 2).
SQ SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFD1CD428 CRC64;

Query Match 16.1%; Score 174; DB 1; Length 1880;
Best Local Similarity 39.0%; Pred. No. 5.58e-13;
Matches 46; Conservative 16; Mismatches 50; Indels 6; Gaps 6;

Db 506 LHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAKYGVKRVAAELLLEDRDHPNAG 565
Qy 16 LATAAARGVEEVALLLEVALPNAPNSYGRPIQVMMX-GSARVAELLHLHGEPNCD 74
Db 566 KNGLT-PLHVAHVHNNLDIVKLLPRGSG-HSP-AWNGYTPFLHIAKQNOVEVARSL 620
Qy 75 PATLTPVHDAAREGFLDTL-VVLHAGARLDVRDAG-GRLPVDLAEELGHRDVARYL 130

RESULT 14
ID ANK1_MOUSE STANDARD; PRT; 1862 AA.
AC Q02357;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ANKYRIN.
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-ERYTHROCYTE;
RX MEDLINE; 92345717.
RA White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
RL regulatory domain";
RL Mamm. genome 3:281-285(1992).
CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
CC NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
CC PLASMA MEMBRANE.
CC -1- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 22 ANK REPEATS.

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CC EMBL; M84756; AAA37236.1; -;
DR HSSP; Q00420; IAWC.
DR MGD; MGI:88024; ANK1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PFAM; PF00023; ank; 23.
DR PFAM; PF00531; death; 1.
DR PFAM; PF00791; ZU5; 1.
KW Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
FT 89 KD DOMAIN (ANION EXCHANGE PROTEIN
FT BINDING DOMAIN).
FT DOMAIN 1 827 89 KD DOMAIN (ANION EXCHANGE PROTEIN
FT BINDING DOMAIN).
FT DOMAIN 828 1386 62 KD DOMAIN (SPECTRIN BINDING
FT DOMAIN).
FT

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FT DOMAIN 1387 1862 55 KD REGULATORY DOMAIN (REGULATES
FT THE BINDING OF ANKYRIN TO SPECTRIN
FT AND THE BAND 3 PROTEIN).
FT 22 X ANK MOTIF REPEATS.
FT 22 X ANK MOTIF 1.
FT 22 X ANK MOTIF 2.
FT 22 X ANK MOTIF 3.
FT 22 X ANK MOTIF 4.
FT 22 X ANK MOTIF 5.
FT 22 X ANK MOTIF 6.
FT 22 X ANK MOTIF 7.
FT 22 X ANK MOTIF 8.
FT 22 X ANK MOTIF 9.
FT 22 X ANK MOTIF 10.
FT 22 X ANK MOTIF 11.
FT 22 X ANK MOTIF 12.
FT 22 X ANK MOTIF 13.
FT 22 X ANK MOTIF 14.
FT 22 X ANK MOTIF 15.
FT 22 X ANK MOTIF 16.
FT 22 X ANK MOTIF 17.
FT 22 X ANK MOTIF 18.
FT 22 X ANK MOTIF 19.
FT 22 X ANK MOTIF 20.
FT 22 X ANK MOTIF 21.
FT 22 X ANK MOTIF 22.
FT DEATH DOMAIN.
FT 1399 1483
SQ SEQUENCE 1862 AA; 204242 MW; AE6B85B529001E5 CRC64;

Query Match 16.0%; Score 173; DB 1; Length 1862;
Best Local Similarity 38.1%; Pred. No. 8.30e-13;
Matches 45; Conservative 17; Mismatches 50; Indels 6; Gaps 6;

Db 503 LHTAAREGHVDTALALLEKEASQACMKTKGFTPLHVAAYKGVRLAELELLEHDAHNPNAAG 562
| ||| ||: |||| | ||: | ||: | ||: | ||: | ||: | ||: | ||: | ||: |
| 16 LATAARGVEVEVRLAEVALPNAAPNSYGRPIQVMM-GSARVAELLHGAEPNCAD 74

Db 563 KNGLT-PLHVAHNNLDIVKLLPRGGSP-HSP-AWNGYTPHLHAAKQNOIEVARSL 617
|| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 75 PATLTRPVHDAAREGFDTL-VLHFRAGARLDVRDAW-GRLPVDLAELGHRDVARYL 130

RESULT 15
ID NTC4_MOUSE STANDARD; PRT; 1964 AA.
AC P31695; Q62389;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING
DE PROTEIN INT-3).
GN NOTCH4 OR INT3 OR INT-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
EN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92194507.
RA Robbins J., Blondel B.J., Callahan D., Callahan R.;
RA "Mouse mammary tumor gene int-3: a member of the notch gene family
RA transforms mammary epithelial cells.";
RL J. Virol. 66:2594-2599(1992).
RN [2]
RN REVISIONS, SEQUENCE FROM N.A.
RX MEDLINE; 97294599.
RA Callahan D., Callahan R.;
RA "The mouse mammary tumor associated gene INT3 is a unique member of
RT the NOTCH gene family (NOTCH4).";
RL Oncogene 14:1883-1890(1997).
RN [3]
RN SEQUENCE FROM N.A.
RX TISSUE-LUNG, AND TESTIS;
RX MEDLINE; 96281668.
RA Uyttendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;

```

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RT Notch4/int-3, a mammary proto-oncogene, is an endothelial
RT cell-specific mammalian Notch gene."
RL Development 122:2251-2259(1996).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DISEASE: ACTIVATED INT-3 TRANSFORMS MAMMARY EPITHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC -1- SIMILARITY: CONTAINS 6 CDC10/SWI6 REPEATS.
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC -----
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CC -----
DR EMBL; M80456; BAB38377.1; -.
DR EMBL; U43691; AAC52630.1; -.
DR PIR; A38072; TVNVT3.
DR HSP; P00740; IIXA.
DR MGD; MGI:107471; NOTCH4.
DR PRINTS; PR00010; EGFBL00D.
DR PROSITE; PS00010; ASX-HYDROXYL; 11.
DR PROSITE; PS00022; EGF_1; 28.
DR PROSITE; PS01186; EGF_2; 21.
DR PROSITE; PS01187; EGF_CA; 9.
DR PFAM; PF00008; EGF; 27.
DR PFAM; PF00023; ank; 6.
DR PFAM; PF00066; notch; 2.
DR PFAM; PF00066; notch; 2.
KW Differentiation; Neurogenesis; Repeat; EGF-like domain; Transmembrane;
KW Glycoprotein; Proto-oncogene; ANK repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 21 1964
FT DOMAIN 21 1443
FT TRANSMEM 1444 1464
FT DOMAIN 1465 1964
FT DOMAIN 21 60
FT DOMAIN 61 112
FT DOMAIN 115 152
FT DOMAIN 153 189
FT DOMAIN 191 229
FT DOMAIN 231 271
FT DOMAIN 273 309
FT DOMAIN 311 350
FT DOMAIN 352 388
FT DOMAIN 389 427
FT DOMAIN 429 470
FT DOMAIN 472 508
FT DOMAIN 510 546
FT DOMAIN 548 584
FT DOMAIN 586 622
FT DOMAIN 622 656
FT DOMAIN 658 686
FT DOMAIN 688 724
FT DOMAIN 726 762
FT DOMAIN 764 800
FT DOMAIN 803 839
FT DOMAIN 841 877
FT DOMAIN 878 924
FT DOMAIN 926 962
FT DOMAIN 964 1000
FT DOMAIN 1002 1040
FT DOMAIN 1042 1081
FT DOMAIN 1083 1122
FT DOMAIN 1126 1167
FT DOMAIN 1168 1282
FT REPEAT 1209 1242
FT REPEAT 1243 1282
FT DOMAIN 1572 1785
FT REPEAT 1572 1603

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MPSEARCH

(TM)

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Mparch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:36:11 2000; Maspar time 18.43 Seconds
Tabular output not generated. 586.937 Million cell updates/sec

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pep
Perfect Score: 1078
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 43.910; Variance 82.660; scale 0.531

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	749	69.5	115	4	Q16361 CELL CYCLE NEGATIVE RE	1.35e-131
2	678	62.9	168	11	P97510 CYCLIN DEPENDENT KINAS	3.53e-116
3	674	62.5	168	11	O89088 CYCLIN DEPENDENT KINAS	2.59e-115
4	621	57.6	102	6	P16/CDKN2A/MTS1 (FRAGM	7.07e-104
5	596	55.3	86	6	Q9X551 P15/MTS2/CDKN2B (FRAGM	1.66e-98
6	566	52.5	86	11	Q921C1 CYCLIN-DEPENDENT KINAS	4.38e-92
7	557	51.7	86	11	O54846 CYCLIN-DEPENDENT KINAS	3.66e-90
8	480	44.5	113	11	Q921C2 CYCLIN-DEPENDENT KINAS	7.77e-74
9	379	35.2	124	13	P70067 CDKN2X PROTEIN.	8.17e-53
10	372	34.5	124	13	Q9W618 P13CDKN2X.	2.22e-51
11	333	30.9	116	4	O95440 CYCLIN-DEPENDENT KINAS	1.89e-43
12	330	30.6	58	6	O97886 CYCLIN-DEPENDENT KINAS	7.63e-43
13	198	18.4	42	11	Q921E8 P15INK4A TUMOR SUPPRES	2.67e-17
14	194	18.0	42	11	Q921C3 CYCLIN-DEPENDENT KINAS	1.42e-16
15	177	16.4	843	11	P97582 ANKYRIN (FRAGMENT).	1.57e-13
16	174	16.1	1719	4	Q13768 ALT. ANKYRIN (VARIANT)	5.32e-13
17	173	16.1	1856	4	O99407 ANKYRIN.	5.32e-13
18	173	16.0	1098	11	O61304 ANKYRIN 1, ERYTHROID (7.97e-13
19	173	16.0	1848	11	O61302 ANKYRIN 1, ERYTHROID (7.97e-13
20	170	15.8	1762	11	O88521 190 KDA ANKYRIN ISOFOR	2.67e-12

21	170	15.8	1943	11	O61307 ANKYRIN 3 (ANKYRIN G)	2.67e-12
22	170	15.8	2622	11	O70511 270 KDA ANKYRIN G ISO	2.67e-12
23	165	15.3	4377	4	Q12955 ANKYRIN G.	1.97e-11
24	163	15.1	44	11	Q921C0 CYCLIN-DEPENDENT KINAS	4.36e-11
25	162	15.0	1095	4	O99458 NOTCH4 (FRAGMENT).	6.48e-11
26	162	15.0	1999	4	O99940 NOTCH4.	6.48e-11
27	162	15.0	2003	4	O00306 NOTCH4.	6.48e-11
28	160	14.8	1435	5	O44997 K12C11.4 PROTEIN.	1.43e-10
29	160	14.8	1786	5	Q17344 UNC-44 (FRAGMENT).	1.43e-10
30	160	14.8	1809	5	Q17487 E. ELEGANS ANKYRIN-REL	1.43e-10
31	160	14.8	1815	5	Q17488 C. ELEGANS ANKYRIN-REL	1.43e-10
32	160	14.8	1867	5	Q17486 C. ELEGANS ANKYRIN-REL	1.43e-10
33	160	14.8	2039	5	Q17489 C. ELEGANS ANKYRIN-REL	1.43e-10
34	160	14.8	6934	5	Q17343 UNC-44 ANKYRINS.	1.43e-10
35	155	14.4	1088	4	Q13484 ANKYRIN G119.	1.01e-09
36	153	14.2	78	4	O15125 ALTERNATIVE SPLICED FO	2.20e-09
37	152	14.1	1549	5	Q24241 ANKYRIN.	3.24e-09
38	149	13.8	835	4	O9Y2V6 HYPOTHETICAL 92.9 KD P	1.03e-08
39	148	13.7	745	4	O9Y544 DJ20208.1 (NOVEL RAT E	1.51e-08
40	146	13.5	837	11	O63618 ESPIN.	3.24e-08
41	146	13.5	1327	4	O95271 TRP1-INTERACTING ANKYR	3.24e-08
42	142	13.2	554	11	O62390 SIMILAR TO MOUSE INT-3	1.47e-07
43	142	13.2	1964	11	O35442 NOTCH4.	1.47e-07
44	140	13.0	882	4	O15084 KIAA0379 (FRAGMENT).	3.13e-07
45	138	12.8	525	11	O9WV72 ANKYRIN REPEAT-CONTAIN	6.60e-07

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	115 AA.
ID	Q16361			
AC	Q16361;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last annotation update)			
DE	CELL CYCLE NEGATIVE REGULATOR BETA FORM (FRAGMENT).			
GN	P16/MTS1/CDKN2			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 95330726.			
RA	STONE S., JIANG P., DAYANANTH P., TAVTIGIAN S.V., KATCHER H.,			
RA	PARRY D., PETERS G., KAMB A.;			
RT	"Complex structure and regulation of the P16 (MTS1) locus.";			
RL	Cancer Res. 55:2988-2994(1995).			
DR	EMBL; S78535; AAC60650.1; -.			
DR	HSSP; P42771; 1BI7.			
FT	NON_TER 1			
SQ	SEQUENCE 115 AA; 12334 MW; F5BEF54B CRC32;			
Query Match	69.5%;	Score 749;	DB 4;	Length 115;
Best Local Similarity	100.0%;	Pred. No. 1.35e-131;		
Matches	107;	Conservative	0;	Mismatches
		Indels	0;	Gaps
Db	9 QVMMGSRVAEELLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDA 68			
QY	50 QVMMGSRVAEELLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDA 109			
Db	69 WGRLPVDAEELGHRDVARYLRAAGTRGSNHARIDAAEGPSDIPD 115			
QY	110 WGRLPVDAEELGHRDVARYLRAAGTRGSNHARIDAAEGPSDIPD 156			
RESULT	2	PRELIMINARY;	PRT;	168 AA.
ID	P97510			
AC	P97510;			
DT	01-MAY-1997 (TrEMBLrel. 03, Created)			
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last annotation update)			
DE	CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR			
DE	PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16, INHIBITS CDK4)			


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Db 121 YLRSA6 126
    |||:|
QY 129 YLRAA6 134

RESULT 4
ID Q9XS51 PRELIMINARY; PRT; 102 AA.
AC Q9XS51;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE P16/CDKN2A/MTS1 (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBMC;
RA OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
RA NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
RT and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010807; BAA33540.1; -.
DR NON_TER 1 1
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 10824 MW; 8C3094E9 CRC32;

Query Match 57.6%; Score 621; DB 6; Length 102;
Best Local Similarity 86.0%; Pred. No. 7.07e-104;
Matches 86; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Db 1 VMMGSAARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVCDAW 60
    |||:|
QY 51 VMMGSAARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVCDAW 110

Db 61 GRPVDLAEEHGRDVARVYLRRAAG 100
    |||:|
QY 111 GRPVDLAEEHGRDVARVYLRRAAGTGRGSHNARIDAAEG 150

RESULT 5
ID Q9XS52 PRELIMINARY; PRT; 86 AA.
AC Q9XS52;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE P15/MTS2/CDKN2B (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBMC;
RA OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
RA NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
RT and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010808; BAA33541.1; -.
DR NON_TER 1 1
FT NON_TER 86 AA; 9340 MW; 8C5D01A0 CRC32;

Query Match 55.3%; Score 596; DB 6; Length 86;
Best Local Similarity 97.6%; Pred. No. 1.66e-98;
Matches 83; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 VMMGSAARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVCDAW 60
    |||:|
QY 51 VMMGSAARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVCDAW 110

Db 61 GRPVDLAEEHGRDVARVYLRRAAG 85
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QY 111 GRPVDLAEEHGRDVARVYLRRAAG 135

RESULT 6
ID Q9Z1C1 PRELIMINARY; PRT; 86 AA.
AC Q9Z1C1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P15.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
RA PELLICER A., FERNANDEZ-PIQUERAS J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79637; AAD00237.1; -.
DR HSSP; P42771; 1B17.
KW Kinase; Cyclin.
FT NON_TER 1 1
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9269 MW; D5811BE2 CRC32;

Query Match 52.5%; Score 566; DB 11; Length 86;
Best Local Similarity 92.9%; Pred. No. 4.38e-92;
Matches 79; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 1 VMMGSAARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVCDAW 60
    |||:|
QY 51 VMMGSAARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVCDAW 110

Db 61 GRPVDLAEEHGRDVARVYLRRAAG 85
    |||:|
QY 111 GRPVDLAEEHGRDVARVYLRRAAG 135

RESULT 7
ID Q54846 PRELIMINARY; PRT; 86 AA.
AC Q54846;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA MALUMBRES M., PELLICER A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015460; AAB94534.1; -.
DR HSSP; P42771; 1B17.
FT NON_TER 1 1
FT NON_TER 86 AA; 9237 MW; FEC97F63 CRC32;

Query Match 51.7%; Score 557; DB 11; Length 86;
Best Local Similarity 91.8%; Pred. No. 3.66e-90;
Matches 78; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 1 VMMGSAARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVCDAW 60
    |||:|
QY 51 VMMGSAARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVCDAW 110

Db 61 GRPVDLAEEHGRDVARVYLRRAAG 85
    |||:|
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OY 136 CTRGSN 141

Search completed: Thu Jul 20 08:36:32 2000
Job time : 21 secs.

MPERCH_PP

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:38:10 2000; MasPar time 6.72 Seconds

Tabular output not generated. 483.073 Million cell updates/sec

Title: >US-09-016-869A-4
Description: (1-137) from US09016869A.pep
Perfect Score: 977
Sequence: 1 MREENKMGPSGGSGDEGLAT.....LAERGHDRVAGYLTATGTD 137

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:geneseq36
l:geneseqp

Statistics: Mean 30.377; Variance 133.757; scale 0.227

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	919	94.1	138	1	R80948 Human multiple tumour	3.58e-75
2	919	94.1	138	1	R81702 Multiple tumour suppressor	3.58e-75
3	919	94.1	138	1	W74553 Amino acid sequence 2	3.58e-75
4	919	94.1	138	1	W80526 A human multiple tumour	3.58e-75
5	919	94.1	138	1	W19255 Human multiple tumour	3.58e-75
6	919	94.1	138	1	W40526 Human MTS2 protein.	3.58e-75
7	907	92.8	138	1	R85117 Cell-cycle regulatory	5.05e-74
8	819	83.8	138	1	R85115 Cell-cycle regulatory	1.33e-65
9	757	77.5	130	1	R85118 Cell-cycle regulatory	1.09e-59
10	749	76.7	130	1	W70823 Mouse multiple tumour	6.31e-59
11	692	70.8	156	1	W19251 Human multiple tumour	1.66e-53
12	692	70.8	156	1	W80524 A human multiple tumour	1.66e-53
13	692	70.8	156	1	W10627 Tumour suppressor p16.	1.66e-53
14	692	70.8	156	1	W74549 Amino acid sequence of	1.66e-53
15	692	70.8	156	1	W40524 Human MTS1 protein.	1.66e-53
16	692	70.8	237	1	W95105 Truncated p27/p16 fusi	1.66e-53
17	692	70.8	252	1	W95103 Truncated p27/p16 fusi	1.66e-53
18	692	70.8	334	1	W95103 Truncated p27/p16 fusi	1.66e-53
19	692	70.8	365	1	W95096 Human p16p27 fusion pr	1.66e-53
20	692	70.8	365	1	W95107 Human p16p27 fusion pr	1.66e-53
21	692	70.8	365	1	W23536 CDK inhibitory fusion	1.66e-53
22	692	70.8	380	1	W95095 Human p16(GS)p27 fusio	1.66e-53
23	692	70.8	380	1	W23535 CDK inhibitory fusion	1.66e-53

ALIGNMENTS

RESULT 1
ID R80948 standard; Protein; 138 AA.

AC R80948;

DT 03-MAY-1996 (first entry)

DE Human multiple tumour suppressor polypeptide, MTS2.

KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;

KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;

KW gene therapy; chronic.

OS Homo sapiens.

PN W09525429-A1.

PD 28-SEP-1995.

PF 17-MAR-1995; U03315.

PR 18-MAR-1994; US-214581.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215088.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI: 95-344401/44.

DR N-PSDB: Q99165.

PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences

PT melanoma or leukaemia

PS Claim 5; Page 103; 156pp; English.

CC Several multiple tumour suppressor (MTS) polypeptides have been

CC isolated and sequenced. This sequence is the MTS polypeptide MTS2.

CC MTS polypeptide-encoding cDNAs and mutants of these are useful for

CC the diagnosis or prognosis of human cancer. Germ-line mutations of

CC MTS cDNAs can be used for diagnosing predisposition to melanoma,

CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's

CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,

CC testis, kidney, stomach and rectum. The wild-type gene is useful

CC for gene therapy and MTS polypeptides may also be used for protein

CC replacement therapy. Also the polypeptides or cells contg. an

CC altered MTS gene are useful for screening for potential cancer

CC therapeutics.

SQ Sequence 138 AA;

Query Match 94.1%; Score 919; DB 1; Length 138;

Best Local Similarity 95.7%; Pred. No. 3.58e-75;

Matches 132; Conservative 3; Mismatches 1; Gaps 1;

DB 1 MREENKMGPSGGSGDEGLASAAARGVLEKVRQLLEAGADPNGVNFRFRRRAIQVNMGSAR 60

|||||

QY 1 MREENKMPGGSGGDEGLATPA-RGLVEKVRHSWEAGADPNCVNFGRRAIQVMMGSGAR 59
 Db 61 VAEILLHLGAEPNCADPATLTRPVHDAAREGFDTLVVHLRAGARLDVRDANGRLPVDLA 120
 QY 60 VAEILLHLGAEPNCADPATLTRPVHDAAREGFDTLVVHLRAGARLDVRDANGRLPVDLA 119
 Db 121 EERGRDVAGYLRTATGD 138
 QY 120 EERGRDVAGYLRTATGD 137

RESULT 2

ID R81702 standard; Protein; 138 AA.
 AC R81702;
 DT 08-MAY-1996 (first entry)
 DE Multiple tumour suppressor 2 (MTS2) polypeptide.
 KW Multiple tumour suppressor; MTS2; cancer; diagnosis; assay;
 KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
 KW pancreas; breast; thyroid.
 OS Homo sapiens.
 PN W09525813-A1.
 PD 28-SEP-1995.
 PF 17-MAR-1995; U03537.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215087.
 PR 18-MAR-1994; US-215086.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 01-JUN-1994; US-251938.
 PA (MYRI-) MYRIAD GENETICS INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 PI Cannon-Albright LA, Kamb A, Skolnick MH;
 DR WPI; 95-344626/44.
 DR N-PSDB; T00745.
 DT Detecting polymorphism associated with cancer pre-disposition - also
 PT DNA, vectors and host cells e.g. for gene or protein replacement
 PT therapy and drug screening
 PS Disclosure: Page 103; 148pp; English.
 CC An individual can be diagnosed as having a predisposition to cancer
 CC by detecting an alteration in the wild type multiple tumour
 CC suppressor (MTS) gene, using gene probes which hybridise to the MTS2
 CC gene ORF T00745 (which encodes R81702). The above assay can also be
 CC used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia
 CC and pancreas, breast and thyroid cancers, etc..
 SQ Sequence 138 AA;

Query Match 94.1%; Score 919; DB 1; Length 138;
 Best Local Similarity 95.7%; Pred. No. 3.58e-75;
 Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPGGSGGDEGLASAAARGLVKVRQLLEAGADPNCVNFGRRAIQVMMGSGAR 60
 QY 1 MREENKMPGGSGGDEGLATPA-RGLVEKVRHSWEAGADPNCVNFGRRAIQVMMGSGAR 59
 Db 61 VAEILLHLGAEPNCADPATLTRPVHDAAREGFDTLVVHLRAGARLDVRDANGRLPVDLA 120
 QY 60 VAEILLHLGAEPNCADPATLTRPVHDAAREGFDTLVVHLRAGARLDVRDANGRLPVDLA 119
 Db 121 EERGRDVAGYLRTATGD 138
 QY 120 EERGRDVAGYLRTATGD 137

RESULT 3

ID W74553 standard; Protein; 138 AA.
 AC W74553;
 DT 04-DEC-1998 (first entry)
 DE Amino acid sequence 2 of the multiple tumour suppressor MTS1E1S.
 KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;
 KW somatic mutation; gene therapy.
 OS Homo sapiens.
 PN US5801236-A.
 PD 01-SEP-1998.
 PF 07-JUN-1995; 480810.

PR 07-JUN-1995; US-480810.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI; 98-494842/42.
 DR N-PSDB; V53831.
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
 PT useful as hybridisation probes, primers and recombinant production
 PT of MTS in the diagnosis and treatment of cancers related to MTS
 PT mutation(s)
 PS Disclosure; Fig 11; 73pp; English.
 CC This is the amino acid sequence of the multiple tumour suppressor
 CC (MTS1E1S) protein, used in the method of the invention. The MTS gene
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by
 CC standard nucleic hybridisation techniques, of patient samples. The
 CC mutated sequences are those that are present in somatic mutations
 CC of the gene in cancers. The vectors can be used for gene therapy
 CC strategies to replace function of mutated protein in patients. These
 CC can also be used to construct protein mimetics, also for therapeutic
 CC strategies. In addition the expression constructs can also be used
 CC for recombinant production of MTS. Recombinant MTS can be used to
 CC screen for drugs to be used for cancer therapy, and the protein
 CC itself may also be used to restore MTS function in a cell.
 SQ Sequence 138 AA;

Query Match 94.1%; Score 919; DB 1; Length 138;
 Best Local Similarity 95.7%; Pred. No. 3.58e-75;
 Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPGGSGGDEGLASAAARGLVKVRQLLEAGADPNCVNFGRRAIQVMMGSGAR 60
 QY 1 MREENKMPGGSGGDEGLATPA-RGLVEKVRHSWEAGADPNCVNFGRRAIQVMMGSGAR 59
 Db 61 VAEILLHLGAEPNCADPATLTRPVHDAAREGFDTLVVHLRAGARLDVRDANGRLPVDLA 120
 QY 60 VAEILLHLGAEPNCADPATLTRPVHDAAREGFDTLVVHLRAGARLDVRDANGRLPVDLA 119
 Db 121 EERGRDVAGYLRTATGD 138
 QY 120 EERGRDVAGYLRTATGD 137

RESULT 4

ID W80526 standard; Protein; 138 AA.
 AC W80526;
 DT 03-FEB-1999 (first entry)
 DE A human multiple tumour suppressor 2 (MTS2) protein.
 KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.
 OS Homo sapiens.
 PN US5843756-A.
 PD 01-DEC-1998.
 PF 28-JUL-1995; 058735.
 PR 28-JUL-1995; US-508735.
 PR 07-JUN-1995; US-487033.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Jiang P, Kamb A, Stone S;
 DR WPI; 99-044585/04.
 DR N-PSDB; W70595.
 PT Mouse multiple tumour suppressor gene segment - useful for primer
 PT design
 PS Example 6; Fig 11; 80pp; English.
 CC The present sequence represents a human multiple tumour suppressor 2
 CC (MTS2) protein. The sequence is homologous to the corresponding
 CC murine gene. Primers designed from the gene can be used to design
 CC primers to detect abnormalities i.e. polymorphisms which may
 CC predispose towards malignancies such as melanoma, leukaemia,
 CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
 CC thyroid, pancreas, uterus and kidneys.

SQ Sequence 138 AA;

Query Match 94.18; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPSSGGSGDEGLASAAAGLVKRYQLLEAGADPNGVNRFRGRRRAIQVMMGSGAR 60
QY 1 MREENKMPSSGGSGDEGLATPA-RGLVEKYRHSWEAGADPNGVNRFRGRRRAIQVMMGSGAR 59

Db 61 VAEALLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 120
QY 60 VAEALLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 119

Db 121 EERGRDVGALYRTATGD 138
QY 120 EERGRDVGALYRTATGD 137

RESULT 5
ID W19255 standard; Protein; 138 AA.
AC W19255;
DT 10-SEP-1997 (first entry)
DE Human multiple tumour suppressor 2 gene product.
KW Human; multiple; tumour; suppressor; MTS2; cancer; diagnosis.
OS Homo sapiens.
PN U55624819-A.
PD 29-APR-1997.
PF 18-MAR-1994; 214582.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003537.
PR 07-JUN-1995; US-474177.
PA (MYRI-) MYRIAD GENETICS INC.
PI (UTAH) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI; 97-258217/23.
DR N-PSDB; T69781.
PT Human mutant multiple tumour suppressor gene sequences - for
PT production of recombinant mutant polypeptide(s)
PS Disclosure; Columns 73-74; 72pp; English.
CC The present sequence the human multiple tumour suppressor 2
CC (MTS2) gene product, useful in cancer diagnosis.
SQ Sequence 138 AA;

Query Match 94.18; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPSSGGSGDEGLASAAAGLVKRYQLLEAGADPNGVNRFRGRRRAIQVMMGSGAR 60
QY 1 MREENKMPSSGGSGDEGLATPA-RGLVEKYRHSWEAGADPNGVNRFRGRRRAIQVMMGSGAR 59

Db 61 VAEALLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 120
QY 60 VAEALLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 119

Db 121 EERGRDVGALYRTATGD 138
QY 120 EERGRDVGALYRTATGD 137

RESULT 6
ID W40526 standard; Protein; 138 AA.
AC W40526;
DT 13-JUL-1998 (first entry)
DE Human MTS2 protein.
KW MTS2; multiple tumour suppressor; diagnosis; cancer;
KW germ-line mutation; familial melanoma locus; MLM; predisposition.
OS Homo sapiens.

PN US5739027-A.
PD 14-APR-1998.
PF 07-JUN-1995; 487033.
PR 07-JUN-1995; US-487033.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
PI WPI; 98-250421/22.
DR N-PSDB; V11250.
PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
PS Disclosure; Fig 11; 72pp; English.
CC This sequence represents a human multiple tumour suppression protein,
CC (MTS2). The MTS gene locus is also referred to as the familial melanoma
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.
SQ Sequence 138 AA;

Query Match 94.18; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPSSGGSGDEGLASAAAGLVKRYQLLEAGADPNGVNRFRGRRRAIQVMMGSGAR 60
QY 1 MREENKMPSSGGSGDEGLATPA-RGLVEKYRHSWEAGADPNGVNRFRGRRRAIQVMMGSGAR 59

Db 61 VAEALLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 120
QY 60 VAEALLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 119

Db 121 EERGRDVGALYRTATGD 138
QY 120 EERGRDVGALYRTATGD 137

RESULT 7
ID R85117 standard; Protein; 138 AA.
AC R85117;
DT 01-MAR-1996 (first entry)
DE Cell-cycle regulatory protein p15.
KW Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
KW CCR; cancer; cell proliferation.
OS Homo sapiens.
PN W09528483-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04636.
PR 14-APR-1994; US-227371.
PR 25-MAY-1994; US-248812.
PR 14-SEP-1994; US-306511.
PR 29-NOV-1994; US-346147.
PA (COLD-) COLD SPRING HARBOR LAB.
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
PI WPI; 95-373798/48.
DR N-PSDB; T02963.
PT New cell cycle regulating proteins bind to cyclin dependent kinase -
PT and related nucleic acids, antibodies etc., used in diagnosis and
PT therapy of abnormal cell proliferation, degeneration etc.
PS Claim 8; Page 78; 109pp; English.
CC The human cell-cycle regulatory (CCR) protein p15 (R85117) was
CC obt'd. by expression of a cDNA clone (T02963) isolated from
CC transforming growth factor-stimulated Hecar cells. CCR p15
CC specifically inhibits the activity of cyclin-dependent kinases
CC during various stages of the cell cycle, and can be used in the
CC treatment and diagnosis of proliferative disorders.

SQ Sequence 138 AA;
Query Match 92.8%; Score 907; DB 1; Length 138;
Best Local Similarity 94.9%; Pred. No. 5.05e-74;
Matches 131; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
Db 1 MREENKMPSPGGSGDEGLATPA-RGLVEKVRHSWEAGADPNVFRGRRRAIQVMMGSGAR 60
QY 1 MREENKMPSPGGSGDEGLATPA-RGLVEKVRHSWEAGADPNVFRGRRRAIQVMMGSGAR 59
Db 61 VAEILLHGAEPNCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLA 120
QY 60 VAEILLHGAEPNCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLA 119
Db 121 EERGRDVGAGYLRATGD 138
QY 120 EERGRDVGAGYLRATGD 137
RESULT 8
ID R85115 standard; Protein; 138 AA.
AC R85115;
DT 01-MAR-1996 (first entry)
DE Cell-cycle regulatory protein p15 homologue.
KW Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
KW CCR; cell proliferation; agonist; antagonist.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_difference 57.59
FT /note= "unidentified amino acids"
FT misc_difference 62
FT /note= "unidentified amino acid"
FT misc_difference 66.67
FT /note= "unidentified amino acids"
FT misc_difference 70.71
FT /note= "unidentified amino acids"
FT misc_difference 74
FT /note= "unidentified amino acid"
FT misc_difference 77
FT /note= "unidentified amino acid"
FT misc_difference 79.81
FT /note= "unidentified amino acid"
FT misc_difference 101.102
FT /note= "unidentified amino acids"
FT misc_difference 117
FT /note= "unidentified amino acid"
FT misc_difference 121
FT /note= "unidentified amino acid"
FT misc_difference 123
FT /note= "unidentified amino acid"
FT misc_difference 126
FT /note= "unidentified amino acid"
FT misc_difference 128.130
FT /note= "unidentified amino acids"
FT misc_difference 134
FT /note= "unidentified amino acid"
FT misc_difference 136
FT /note= "unidentified amino acid"
PN W09528483-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04636.
PR 14-APR-1994; US-227371.
PR 25-MAY-1994; US-248812.
PR 14-SEP-1994; US-306511.
PR 29-NOV-1994; US-346147.
PA (COLD-) COLD SPRING HARBOR LAB.
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
DR WPI; 95-373798/48.
PT New cell cycle regulating proteins bind to cyclin dependent kinase -
and related nucleic acids, antibodies etc., used in diagnosis and
therapy of abnormal cell proliferation, degeneration etc.
PS Claim 16; Page 87-88; 109pp; English.
CC A homologue (R85115) of the human cell-cycle regulatory (CCR) protein

CC p15, showing at least 60% homology to p15 (R85117), functions as either
an agonist or antagonist of cell cycle regulation.
SQ Sequence 138 AA;
Query Match 83.8%; Score 819; DB 1; Length 138;
Best Local Similarity 82.6%; Pred. No. 1.33e-65;
Matches 114; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
Db 1 MREENKMPSPGGSGDEGLATPA-RGLVEKVRHSWEAGADPNVFRGRRRAIQVMMGSGARV 60
QY 1 MREENKMPSPGGSGDEGLATPA-RGLVEKVRHSWEAGADPNVFRGRRRAIQVMMGSGARV 60
Db 61 AXLLXXGAXXNCXDPXTXXRPVPHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLA 120
QY 61 AELLLLHGAEPNCADPATLT-RPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLA 119
Db 121 XEXGHDXDXXYLRXAXGD 138
QY 120 EERGRDVGAGYLRATGD 137
RESULT 9
ID R85118 standard; Protein; 130 AA.
AC R85118;
DT 01-MAR-1996 (first entry)
DE Cell-cycle regulatory protein p15.
KW Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
KW CCR; cancer; cell proliferation.
OS Mus sp.
PN W09528483-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04636.
PR 14-APR-1994; US-227371.
PR 25-MAY-1994; US-248812.
PR 14-SEP-1994; US-306511.
PR 29-NOV-1994; US-346147.
PA (COLD-) COLD SPRING HARBOR LAB.
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
DR WPI; 95-373798/48.
PT New cell cycle regulating proteins bind to cyclin dependent kinase -
and related nucleic acids, antibodies etc., used in diagnosis and
therapy of abnormal cell proliferation, degeneration etc.
PS Claim 9; Page 81-82; 109pp; English.
CC The mouse cell-cycle regulatory (CCR) protein p15 (R85118) was
obtained by expression of a cDNA clone (T02964) isolated from
mouse embryonal carcinoma cells. CCR p15 specifically inhibits the
activity of cyclin-dependent kinases during various stages of the
cell cycle, and can be used in the treatment and diagnosis of
proliferative disorders.
SQ Sequence 130 AA;
Query Match 77.5%; Score 757; DB 1; Length 130;
Best Local Similarity 85.9%; Pred. No. 1.09e-59;
Matches 110; Conservative 10; Mismatches 7; Indels 1; Gaps 1;
Db 3 GGSSDAGLATPAARGQVETVQQLLEAGADPNALNFRGRRRAIQVMMGSGARVAELLHGA 62
QY 11 GGSDEGLATPA-RGLVEKVRHSWEAGADPNVFRGRRRAIQVMMGSGARVAELLHGA 69
Db 63 EPNCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAEEQGRDTR 122
QY 70 EPNCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAEEGRDTR 129
Db 123 YLHAATGD 130
QY 130 YLRTATGD 137
RESULT 10
ID W08223 standard; Protein; 130 AA.
AC W08223;
DT 03-FEB-1999 (first entry)

DE Mouse multiple tumour suppressor 2 (MTS2) protein.
 KW Murine; multiple tumour suppressor 2 gene; MTS2; cancer.
 OS Mus musculus.
 PN 01-DEC-1998. PD 058735.
 PF 28-JUL-1995; US-508735.
 PR 28-JUL-1995; US-508735.
 PR 07-JUN-1995; US-487033.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Jiang P, Kamb A, Stone S;
 DR WPI: 99-044585/04.
 DR N-PSDB: V70624.
 PT Mouse multiple tumour suppressor gene segment - useful for primer
 PT design

PS Example 7; Fig 19; 80pp; English.
 CC The present sequence represents mouse multiple tumour suppressor 2
 CC (MTS2) gene. The MTS1 gene can be used to design primers to
 CC detect abnormalities i.e. polymorphisms which may predispose
 CC towards malignancies such as melanoma, leukaemia, astrocytoma,
 CC lymphoma, glioma, as well as tumours of e.g. the breast,
 CC thyroid, pancreas, uterus and kidneys.
 CC Sequence 130 AA;
 SQ

Query Match 76.7%; Score 749; DB 1; Length 130;
 Best Local Similarity 85.2%; Pred. No. 6.31e-59;
 Matches 109; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

Db 3 GGSADGATPAARGVETVQLLEAGADPNALNRRGRRPQVMMGSAQVAELLHGA 62
 QY 11 GGSDEGLATPA-RGLVEKVRHWEAGADPNVRRFARRAIQVMMGSAQVAELLHGA 69
 Db 63 EPCADPATITRPVHDAAREGFLDTLVVLRHAGARLDVCDWAGRLPVDLAEERHDIAR 122
 QY 70 EPCADPATITRPVHDAAREGFLDTLVVLRHAGARLDVCDWAGRLPVDLAEERHDIAR 129
 Db 123 YLHAATGD 130
 QY 130 YLHAATGD 137

RESULT 11
 ID W19251 standard; Protein; 156 AA.
 AC W19251;
 DT 10-SEP-1997 (first entry)
 DE Human multiple tumour suppressor 1 gene product.
 KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
 OS Homo sapiens.
 PN US5624819-A.
 PD 29-APR-1997.
 PF 18-MAR-1994; 214582.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-003537.
 PR 07-JUN-1995; US-474177.
 PA (MYRI-) MYRIAD GENETICS INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 PI Cannon-Albright LA, Kamb A, Skolnick MH;
 DR WPI: 97-258217/23.
 DR N-PSDB: T72311.
 PT Human mutant multiple tumour suppressor gene sequences - for
 PT production of recombinant mutant polypeptide(s)
 PS Claim 1; Columns 61-64; 72pp; English.
 CC The present sequence the human multiple tumour suppressor 1
 CC (MTS1) gene product, useful in cancer diagnosis.
 CC Sequence 156 AA;

Query Match 70.8%; Score 692; DB 1; Length 156;
 Best Local Similarity 85.8%; Pred. No. 1.66e-53;
 Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Db 16 LATAAARGVEEVYRALLEAGALPNAPNSYGRRTQVMMGSAQVAELLHGAEPNCADP 75
 QY 18 LATPA-RGLVEKVRHWEAGADPNVRRFARRAIQVMMGSAQVAELLHGAEPNCADP 76
 Db 76 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVCDWAGRLPVDLAEERHDIAR 135
 QY 77 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVCDWAGRLPVDLAEERHDIAR 136

RESULT 12

ID W80524 standard; Protein; 156 AA.
 AC W80524;
 DT 03-FEB-1999 (first entry)
 DE A human multiple tumour suppressor 1 (MTS1) protein.
 KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.
 OS Homo sapiens.
 PN US5843756-A.
 PD 01-DEC-1998.
 PF 28-JUL-1995; 058735.
 PR 28-JUL-1995; US-508735.
 PR 07-JUN-1995; US-487033.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Jiang P, Kamb A, Stone S;
 DR WPI: 99-044585/04.
 DR N-PSDB: V70583.
 PT Mouse multiple tumour suppressor gene segment - useful for primer
 PT design

PS Disclosure; Columns 65-66; 80pp; English.
 CC The present sequence represents a human multiple tumour suppressor 1
 CC (MTS1) protein. The sequence is homologous to the corresponding
 CC murine gene. Primers designed from the gene can be used to design
 CC primers to detect abnormalities i.e. polymorphisms which may
 CC predispose towards malignancies such as melanoma, leukaemia,
 CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
 CC thyroid, pancreas, uterus and kidneys.
 CC Sequence 156 AA;
 SQ

Query Match 70.8%; Score 692; DB 1; Length 156;
 Best Local Similarity 85.8%; Pred. No. 1.66e-53;
 Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Db 16 LATAAARGVEEVYRALLEAGALPNAPNSYGRRTQVMMGSAQVAELLHGAEPNCADP 75
 QY 18 LATPA-RGLVEKVRHWEAGADPNVRRFARRAIQVMMGSAQVAELLHGAEPNCADP 76
 Db 76 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVCDWAGRLPVDLAEERHDIAR 135
 QY 77 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVCDWAGRLPVDLAEERHDIAR 136

RESULT 13

ID W10627 standard; Protein; 156 AA.
 AC W10627;
 DT 28-OCT-1997 (first entry)
 DE Tumour suppressor p16.
 KW Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;
 KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
 KW anti-angiogenic activity; hyperproliferative disorder.
 OS Homo sapiens.
 PN WO9703635-A2.
 PD 06-FEB-1997.
 PF 17-JUL-1996; U11787.
 PR 17-JUL-1995; US-502881.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Jin X, Roth J;
 DR WPI: 97-132336/12.
 DR N-PSDB: T60951.
 PT Expression construct contg. DNA for tumour suppressor p16 - to
 PT restore p16 activity to transformed cells, useful for treating lung
 PT or bladder cancer or melanoma
 PS Disclosure; Fig 1b; 92pp; English.
 CC This sequence represents the tumour suppressor p16. The DNA encoding
 CC this sequence is joined to a promoter functional in eukaryotic cells and

used in the expression construct of the invention. p16 is an inhibitory subunit, which is involved in the control of cyclin-dependent kinase 4 activity, and functions as a tumour suppressor. By detecting this sequence or the DNA encoding it, cancer cells can be detected. When the nucleic acid molecule is in the sense orientation, the expression construct can be used to restore p16 function in a cell, particularly by reversing the transformed phenotype in tumours, especially lung or bladder cancer or melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the nucleic acid molecule is inserted in the antisense orientation, the expression construct inhibits p16 function. Reduced or increased levels of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by Southern or Northern blot, antibody immunoblot, fluorescent cell sorting or immunoassay.

Sequence 156 AA;

Query Match 70.8%; Score 692; DB 1; Length 156;
Best Local Similarity 85.8%; Pred. No. 1.66e-53;
Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Db 16 LATAAARGVEEVALLLEAGALPNAPNSYGRPIQVMMGSAEVLHLLHGAEPNCADP 75
QY 18 LATPA-RGLVEKVRHSWEAGADPNVRFGRRAIQVMMGSAEVLHLLHGAEPNCADP 76
Db 76 ATLTPVHDAAREGLDVLVLRHAGARLDVWDAGRLPVDLAELGHRDVARYLRAAG 135
QY 77 ATLTPVHDAAREGLDVLVLRHAGARLDVWDAGRLPVDLAELGHRDVARYLRTATG 136

RESULT 14

ID: W74549 standard; Protein; 156 AA.

AC W74549;
DT 04-DEC-1998 (first entry)
DE Amino acid sequence of multiple tumour suppressor 1.
KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
KW somatic mutation; gene therapy.
OS Homo sapiens.
PN US5801236-A.
PD 01-SEP-1998.
PF 07-JUN-1995; 480810.
PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A.

DR WPI: 98-494842/42.

DR N-PSDB; V53819.

PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)

PS Disclosure; Column 63-64; 73pp; English.

CC This is the amino acid sequence of the multiple tumour suppressor 1
CC (MTS-1) protein, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer, e.g. by
CC standard nucleic acid hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.

Sequence 156 AA;

Query Match 70.8%; Score 692; DB 1; Length 156;
Best Local Similarity 85.8%; Pred. No. 1.66e-53;
Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Db 16 LATAAARGVEEVALLLEAGALPNAPNSYGRPIQVMMGSAEVLHLLHGAEPNCADP 75
QY 18 LATPA-RGLVEKVRHSWEAGADPNVRFGRRAIQVMMGSAEVLHLLHGAEPNCADP 76
Db 76 ATLTPVHDAAREGLDVLVLRHAGARLDVWDAGRLPVDLAELGHRDVARYLRAAG 135
QY 77 ATLTPVHDAAREGLDVLVLRHAGARLDVWDAGRLPVDLAELGHRDVARYLRTATG 136

RESULT 15

ID: W40524 standard; Protein; 156 AA.

AC W40524; 1998 (first entry)

DE Human MTS1 protein.

KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
KW familial melanoma locus; MLM; predisposition.
OS Homo sapiens.

PN US5739027-A.

PD 14-APR-1998.

PF 07-JUN-1995; 487033.

PR 07-JUN-1995; US-487033.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PR 17-MAR-1995; WO-003316.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A.

DR WPI: 98-250421/22.

DR N-PSDB; V11238.

PT DNA specific for Multiple Tumour Suppressor 1b1-beta gene - are

PT useful for the diagnosis of cancers related to MTS1b1-beta

PT mutation(s) and their treatment

PS Disclosure; Column 63-64; 72pp; English.

CC This sequence represents a human multiple tumour suppression protein,
CC MTS1. The MTS gene locus is also referred to as the familial melanoma
CC (FML) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.

CC Sequence 156 AA;

Query Match 70.8%; Score 692; DB 1; Length 156;

Best Local Similarity 85.8%; Pred. No. 1.66e-53;

Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Db 16 LATAAARGVEEVALLLEAGALPNAPNSYGRPIQVMMGSAEVLHLLHGAEPNCADP 75
QY 18 LATPA-RGLVEKVRHSWEAGADPNVRFGRRAIQVMMGSAEVLHLLHGAEPNCADP 76
Db 76 ATLTPVHDAAREGLDVLVLRHAGARLDVWDAGRLPVDLAELGHRDVARYLRAAG 135
QY 77 ATLTPVHDAAREGLDVLVLRHAGARLDVWDAGRLPVDLAELGHRDVARYLRTATG 136

Search completed: Thu Jul 20 08:38:18 2000

Job time : 8 secs.

CC LENGTH: 136 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..136
CC OTHER INFORMATION: /note= "human p15"
SQ SEQUENCE 136 AA; 14689 MW; 79498 CN;

Query Match 98.2%; Score 959; DB 4; Length 136;
Best Local Similarity 99.38; Pred. No. 1.06e-77;
Matches 136; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 MREENKMGPSGGSGDE-LATPARGLVKVRHSWEAGADPNGVNRFGRRRAIQVMMGSGARV 59
QY 1 MREENKMGPSGGSGDEGLATPARGLVKVRHSWEAGADPNGVNRFGRRRAIQVMMGSGARV 60
Db 60 AELLHLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAE 119
QY 61 AELLHLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
Db 120 ERGRDVGAGYLRTATGD 136
QY 121 ERGRDVGAGYLRTATGD 137

RESULT 4
ID PCT-US95-04636-4 STANDARD; PRT; 138 AA.
XX XXXXXX
AC XXXXXX
XX XXXXXX
DT XXXXXX
XX XXXXXX
DE XXXXXX
XX XXXXXX
CC Sequence 4, Application PC/TUS9504636
CC Sequence 4, Application PC/TUS9504636
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
CC TITLE OF INVENTION: Related Thereto
CC NUMBER OF SEQUENCES: 10
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Ascii(text)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/04636
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/346,147
CC FILING DATE: 29-NOV-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/306,511
CC FILING DATE: 14-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/248,812
CC FILING DATE: 25-MAY-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,371
CC FILING DATE: 14-APR-1994
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;

Query Match 94.1%; Score 919; DB 4; Length 138;

Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMGPSGGSGDEGLASAAARGLVKVRQLLEAGADPNGVNRFGRRRAIQVMMGSGAR 60
QY 1 MREENKMGPSGGSGDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRRAIQVMMGSGAR 59
Db 61 VAELLHLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLA 120
QY 60 VAELLHLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLA 119
Db 121 ERGRDVGAGYLRTATGD 138
QY 120 ERGRDVGAGYLRTATGD 137

RESULT 5
ID US-09-120-130-16 STANDARD; PRT; 138 AA.
XX XXXXXX
AC XXXXXX
XX XXXXXX
DT XXXXXX
XX XXXXXX
DE XXXXXX
XX XXXXXX
CC Sequence 16, Application US/09120130
CC Sequence 16, Application US/09120130
CC Patent No. 6037462
CC GENERAL INFORMATION:
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS1 GENE
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/120,130
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/480,810
CC FILING DATE:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,087
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,086
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/214,582
CC FILING DATE: 18-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Innen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:

CC PRIOR APPLICATION DATA: US 08/251,938
CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,087
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,086
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/214,582
CC FILING DATE: 18-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348-B
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;

Query Match 94.1%; Score 919; DB 2; Length 138;
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPGGSGGDEGLASAAAGLVKVRQLLEAGADPNVNRFGRRRAIQVNMMSGAR 60
QY 1 MREENKMPGGSGGDEGLATPA-RGLVEKYRHSWEAGADPNVNRFGRRRAIQVNMMSGAR 59
Db 61 VAEILLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 120
QY 60 VAEILLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 119
Db 121 EERGRDVGAGLYRTATGD 138
QY 120 EERGRDVGAGLYRTATGD 137

RESULT 8
ID US-08-508-735-16 STANDARD; PRT; 138 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
Sequence 16, Application US/08508735
XX
Sequence 16, Application US/08508735
CC Patent No. 5843756
CC GENERAL INFORMATION:
CC APPLICANT: Stone, Steven
CC APPLICANT: Jiang, Ping
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
CC NUMBER OF SEQUENCES: 47
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM: Floppy disk
CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/508,735
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US to be assigned
CC FILING DATE: 07-JUN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/03316
CC FILING DATE: 17-MAR-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4848
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;

Query Match 94.1%; Score 919; DB 2; Length 138;
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPGGSGGDEGLASAAAGLVKVRQLLEAGADPNVNRFGRRRAIQVNMMSGAR 60
QY 1 MREENKMPGGSGGDEGLATPA-RGLVEKYRHSWEAGADPNVNRFGRRRAIQVNMMSGAR 59
Db 61 VAEILLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 120
QY 60 VAEILLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 119
Db 121 EERGRDVGAGLYRTATGD 138
QY 120 EERGRDVGAGLYRTATGD 137

RESULT 9
ID US-08-480-810-16 STANDARD; PRT; 138 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
Sequence 16, Application US/08480810
XX
Sequence 16, Application US/08480810
CC Patent No. 5801236
CC GENERAL INFORMATION:
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS1 GENE
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM: Floppy disk
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:

CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/848,251
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/474,083
CC FILING DATE: 07-JUN-1995
CC APPLICATION NUMBER: PCT/US95/03537
CC FILING DATE: 17-MAR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,087
CC FILING DATE: 18-MAR-1994
CC APPLICATION NUMBER: US 08/215,086
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/214,582
CC FILING DATE: 18-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348-G
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;

Query Match 94.1%; Score 919; DB 2; Length 138;
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Db 1 MREENKMGPSGGSDGLASAAAGLVKVRQLLEAGADPNVNRFGRRRAIQVMMGSGAR 60
Qy 1 MREENKMGPSGGSDGLATPA-RGLVEKVRHSEAGADPNVNRFGRRRAIQVMMGSGAR 59
Db 61 VAEILLHGAEPNCADPATLTFRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLA 120
Qy 60 VAEILLHGAEPNCADPATLTFRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLA 119
Db 121 EERGRDVAGYLRTATGD 138
Qy 120 EERGRDVAGYLRTATGD 137

RESULT 14
ID US-08-487-033-16 STANDARD; PRT; 138 AA.
XX
AC xxxxxx
XX
DT
XX
DE

XX Sequence 16, Application US/08487033
CC Patent No. 5739027
CC GENERAL INFORMATION:
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS1E1-Beta GENE
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/487,033
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/03316
CC FILING DATE: 17-MAR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,087
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,086
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/214,582
CC FILING DATE: 18-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348-C
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;
Query Match 94.1%; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Db 1 MREENKMGPSGGSDGLASAAAGLVKVRQLLEAGADPNVNRFGRRRAIQVMMGSGAR 60
Qy 1 MREENKMGPSGGSDGLATPA-RGLVEKVRHSEAGADPNVNRFGRRRAIQVMMGSGAR 59
Db 61 VAEILLHGAEPNCADPATLTFRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLA 120
Qy 60 VAEILLHGAEPNCADPATLTFRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLA 119
Db 121 EERGRDVAGYLRTATGD 138
Qy 120 EERGRDVAGYLRTATGD 137

W P E R L H (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:38:35 2000; MapPar time 10.90 Seconds
592.803 Million cell updates/sec

Tabular output not generated.

Title: >US-09-016-869A-4
Description: (1-137) from US09016869A.pap
Perfect Score: 977
Sequence: 1 MREKNKMGPMGGSGDEGLAT.....LAERGRHVRVAGYLRATGTD 137

Scoring table: PAM 150
Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir63
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 42.515; Variance 86.121; scale 0.494

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	919	94.1	138	2 B55479	CDK4 inhibitor p14(INK4B)	7.51e-158
2	749	76.7	130	2 I78845	p15INK4b - mouse	3.56e-123
3	692	70.8	156	2 J20141	cyclin dependent kina	1.22e-111
4	581	59.5	167	2 I58352	p16INK4a - mouse	2.36e-89
5	329	33.7	164	2 A57378	cyclin-dependent kina	3.08e-40
6	315	32.2	166	2 A57379	CDK4/CDK6 inhibitor p	1.30e-37
7	312	31.9	166	2 B57378	cyclin-dependent kina	4.74e-37
8	284	29.1	41	2 I52720	gene p15INK4B protein	7.40e-32
9	249	25.5	168	2 A55479	CDK6 inhibitor p18 -	1.74e-25
10	247	25.3	168	2 B57379	CDK4/CDK6 inhibitor p	3.99e-25
11	140	14.3	1423	1 I37275	death-associated prot	4.79e-07
12	140	14.3	1856	2 B35049	ankyrin 1, erythrocyt	4.79e-07
13	140	14.3	1880	2 A35049	ankyrin 1, erythrocyt	4.79e-07
14	140	14.3	1881	1 S3HUK	ankyrin 1, erythrocyt	4.79e-07
15	137	14.0	1848	2 S37771	ankyrin, erythrocyte	1.38e-06
16	137	14.0	1862	2 I49502	ankyrin - mouse	1.38e-06
17	133	13.6	2524	2 A35844	otch protein - Afric	5.56e-06
18	132	13.5	4377	2 A35575	ankyrin 3, long splic	7.86e-06
19	131	13.4	3924	2 S37431	ankyrin 2, neuronal	1.11e-05
20	130	13.3	2531	2 S18188	otch protein homolog	1.56e-05
21	129	13.2	1411	2 S30355	alpha-latroinsectotox	2.20e-05
22	129	13.2	2318	2 S45306	otch 3 protein - mou	2.20e-05
23	129	13.2	2555	2 A40043	otch protein homolog	2.20e-05

24	128	13.1	2437	2 S42612	transmembrane protein	3.10e-05
25	127	13.0	2321	2 S78549	otch3 protein - huma	4.36e-05
26	125	12.8	2531	2 A46019	otch1 protein - mou	8.58e-05
27	123	12.6	638	2 A56695	otch2 protein homolo	1.68e-04
28	123	12.6	249128	2 I49128	cell-fate determining	1.68e-04
29	122	12.5	677	2 I49045	SKD3 - mouse	2.35e-04
30	121	12.4	209	2 T15888	hypothetical protein	3.27e-04
31	118	12.1	323	2 B47159	ankyrin-like repeat p	8.82e-04
32	118	12.1	2703	1 A24420	otch protein - fruit	8.82e-04
33	115	11.8	414	2 A53950	transcription factor	2.35e-03
34	115	11.8	1964	2 T09059	otch4 - mouse	2.35e-03
35	114	11.7	1786	2 A57282	ankyrin-related prote	3.25e-03
36	114	11.7	1809	2 T15345	ankyrin-related unc-4	3.25e-03
37	114	11.7	1815	2 T15346	elegans ankyrin-relat	3.25e-03
38	114	11.7	1867	2 T15344	ankyrin-related unc-4	3.25e-03
39	114	11.7	2039	2 T15347	ankyrin-related unc-4	3.25e-03
40	111	11.4	1001	2 S30385	G9a protein - human	8.49e-03
41	110	11.3	934	1 H71274	probable ankyrin - sy	1.17e-02
42	108	11.1	249	2 S77600	probable fnr-like tra	2.19e-02
43	108	11.1	446	2 A34794	B-cell CLL/lymphoma 3	2.19e-02
44	106	10.8	1549	2 T13940	ankyrin - fruit fly (4.09e-02
45	103	10.5	971	2 A35697	transcription factor	1.03e-01

ALIGNMENTS

RESULT	1	B55479	#type complete
ENTRY		CDK4 inhibitor p14(INK4B/MTS2) - human	
TITLE		CDK6-associated protein p15(INK4B); cyclin-dependent kinase	
ALTERNATE_NAMES		inhibitor 2B; multiple tumor suppressor 2	
ORGANISM		#formal_name Homo sapiens #common_name man	
DATE		23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change	
ACCESSIONS		B55479; S47593; I81183; I52713	
REFERENCE		Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.; Xiong, Y. Genes Dev. (1994) 8:2939-2952	
#authors		Growth suppression by p18, a p16(INK4/MTS1)- and p14 (INK4B/MTS2)-related CDK6 inhibitor, correlates with wild-type pRB function.	
#journal		#cross-references MUID:9505079	
#title		#accession B55479	
#cross-references		#molecule_type mRNA	
#accession		#residues 1-138 #label GUA	
#molecule_type		##cross-references GB:U17075; NID:9639715; PID:9639716	
#residues		##experimental_source HeLa cells	
REFERENCE		S47593	
#authors		Hannon, G.J.; Beach, D.	
#journal		Nature (1994) 371:257-261	
#title		p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.	
#cross-references		MUID:94359613	
#accession		S47593	
#molecule_type		mRNA	
#residues		1-19, 'tp', 22, 24-31, 'HSW', 35-138 #label HAN	
##cross-references		GB:L36844; NID:9556197; PIDN:AAA50282.1; PID:9556198	
##experimental_source		HaCat cells	
REFERENCE		I59585	
#authors		Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.; Johnson, B.E.; Skolnick, M.H.	
#journal		Science (1994) 264:436-440	
#title		A cell cycle regulator potentially involved in genesis of many tumor types.	
#cross-references		MUID:94204645	
#accession		I81183	
#status		translation not shown; translated from GB/EMBL/DBJ	
#molecule_type		DNA	
#residues		53-138 #label KAM	
#cross-references		GB:S69805; NID:9546273	
REFERENCE		I52713	

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#authors      Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.;
Papadopoulos, N.; Markowitz, S.; Willson, J.K.; Kinzler,
K.W.; Vogelstein, B.
#journal      Cancer Res. (1994) 54:6353-6358
#title        Deletion of p16 and p15 genes in brain tumors.
#cross-references MUID:95079408
#accession    152713
#status       preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues     1-52 ##label RES
#cross-references GB:S75756; NID:g861470
GENETICS
#gene         GDB:CDKN2B; MTS2
#cross-references GDB:S75757; OMIM:600431
#map_position 9p21-9p21
KEYWORDS      cell cycle control; protein kinase inhibitor; tumor
suppressor
SUMMARY       #length 138 #molecular-weight 14722 #checksum 1236
Query Match   94.1%; Score 919; DB 2; Length 138;
Best Local Similarity 95.7%; Pred. No. 7.51e-158;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Db 1 MREENKMGPSGGSDGLASAAAGLVKVRQLLEAGADPVGNGRRAIQVMMGSGAR 60
QY 1 MREENKMGPSGGSDGLATPA-RGLVKRVSWEGADPVGNGRRAIQVMMGSGAR 59
Db 61 VAEILLHGAEPNCADPATLPVPVHDAAREGFLDTLVLHRRAGALDVRDANGRLPVDLA 120
QY 60 VAEILLHGAEPNCADPATLPVPVHDAAREGFLDTLVLHRRAGALDVRDANGRLPVDLA 119
Db 121 EERGHDRVAGYLRTATGD 138
QY 120 EERGHDRVAGYLRTATGD 137
RESULT 2
ENTRY   I78845 #type complete
TITLE   p15INK4b - mouse
ORGANISM #formal_name Mus sp. #common_name mouse
DATE     02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
28-Feb-1997
ACCESSIONS I78845
REFERENCE   Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.;
Trono, D.; Richter, K.H.; Walker, C.; Beach, D.; Sherr,
C.J.; Serrano, M.
#journal    Oncogene (1995) 11:635-645
#title      Cloning and characterization of murine p15INK4a and p15INK4b
genes.
#cross-references MUID:95380169
#accession  I78845
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues    1-130 ##label RES
#cross-references GB:S79252; NID:gl087092; PID:gl087093
GENETICS
#gene        p15INK4b
SUMMARY      #length 130 #molecular-weight 13788 #checksum 7879
Query Match   76.7%; Score 749; DB 2; Length 130;
Best Local Similarity 85.2%; Pred. No. 3.56e-123;
Matches 109; Conservative 11; Mismatches 7; Indels 1; Gaps 1;
Db 3 GGSDDAGLATAARGQVETVROLLEAGADPNALNFRGRIQVMMGSAQVAELLLHGA 62
QY 11 GGSDEGLATPA-RGLVKRVSWEGADPVGNGRRAIQVMMGSAQVAELLLHGA 69
Db 63 EPNCADPATLPVPVHDAAREGFLDTLVLHRRAGALDVRDANGRLPVDLAEEQGHRIAR 122
QY 70 EPNCADPATLPVPVHDAAREGFLDTLVLHRRAGALDVRDANGRLPVDLAEEQGHRIAR 122
Db 123 YLHAATGD 130
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QY 130 YLRTATGD 137
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RESULT 3
ENTRY   JE0141 #type complete
TITLE   cyclin dependent kinase - human
ALTERNATE_NAMES CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase
inhibitor 2A; multiple tumor suppressor 1 (MTS1)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change
26-Aug-1999
ACCESSIONS JE0141; I59268; S39359; I59585; JC5679
REFERENCE   JE0141
#authors    Huang, C.G.; Deng, W.; Fu, J.L.
#journal    Chinese J. Biotechnol. (1997) 13:105-107
#title      Molecular cloning and sequencing of p16ink4 cDNA from hela
cell.
#accession  JE0141
#molecule_type mRNA
#residues   1-156 ##label HUA
#experimental_source Hella cell
REFERENCE   I59268
#authors    Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.;
Serrano, M.; Bennett, W.P.; Forrester, K.; Gerwin, B.;
Hussain, S.P.; Beach, D.H.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:11045-11049
#title      Mutations and altered expression of p16INK4 in human cancer.
#cross-references MUID:95062202
#accession  I59368
#status      translation not shown; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues   1-152 ##label RES
#cross-references GB:S74232; NID:g710467
#note       this report is a correction
REFERENCE   S39359
#authors    Serrano, M.; Hannon, G.J.; Beach, D.
#journal    Nature (1993) 366:704-707
#title      A new regulatory motif in cell-cycle control causing specific
inhibition of cyclin D/CDK4.
#cross-references MUID:94081956
#accession  S39359
#status      preliminary
#molecule_type mRNA
#residues   9-34, 'V' 36-156 ##label SER
#note       this sequence has been corrected in reference I59268
REFERENCE   I59585
#authors    Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.;
Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.;
Johnson, B.E.; Skolnick, M.H.
#journal    Science (1994) 264:436-440
#title      A cell cycle regulator potentially involved in genesis of
many tumor types.
#cross-references MUID:94204645
#accession  I59585
#status      translation not shown; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues   51-152 ##label RE2
#cross-references GB:S69804; NID:g546272
REFERENCE   JC5679
#authors    Huang, C.; Deng, W.; Fu, J.
#journal    Chinese J. Biotechnol. (1997) 13:105-107
#title      Molecular cloning and sequencing of p16 ink4 cDNA from hela
cell.
#accession  JC5679
#molecule_type mRNA
#residues   1-156 ##label HU2
#note       This protein suppresses the function of cyclin D1/CDK4 and cyclin
D1/CDK6.
GENETICS
#gene        p16ink4; MLM; CDKN2; MTS1
#cross-references GDB:335362; GDB:CDKN2A; OMIM:600160
#map_position 9p21-9p21
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[illegible]

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#accession B57378 #molecule_type preliminary
#status 1-166 #label CHA
#residues 1-166 #label CHA
#cross-references GB:U20497; NID:G791204; PID:G791205
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology
SUMMARY #length 166 #molecular-weight 17920 #checksum 3767

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Best Local Similarity 47.4%; Pred. No. 4.74e-37;
Matches 54; Conservative 20; Mismatches 38; Indels 2; Gaps 2;

Db 14 GARGDQVQVRLRLHRLVDPDALNRGKALQVMMFGSPAVALELLKQGASPNVDAS 73
QY 19 ATPARGLVKVRHWEAG-ADPNQVNRGRRRAIQVMMGSRVAEALLLHGAEPNCADPA 77
Db 74 G-TSPVHDAARTGFLDTLKVLEHGADYNALDSTGSLPIHLAIREGHSSVVSFL 126
QY 78 TLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAERGHDRVAGYL 131

RESULT 8
ENTRY #type fragment
TITLE gene p15INK4B protein - rat (fragment)
ORGANISM #formal_name Rattus sp. #common_name rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS I52720
REFERENCE Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.
#journal Cancer Res. (1995) 55:1607-1612
#title Association of rat p15INK4B/p16INK4 deletions with monosomy 5
in kidney epithelial cell lines but not primary renal
tumors.
#cross-references MUID:95228036
#accession I52720
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-41 #label RES
#cross-references GB:S77734; NID:G998711
GENETICS
#gene p15INK4B
#length 41 #checksum 3296
SUMMARY

Query Match 29.1%; Score 284; DB 2; Length 41;
Best Local Similarity 97.6%; Pred. No. 7.40e-32;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGSAQVAEALLLHGAEPNCADPATLTPRVHDAAREGFLD 41
QY 53 MMGSAQVAEALLLHGAEPNCADPATLTPRVHDAAREGFLD 93

RESULT 9
ENTRY #type complete
TITLE CDK6 inhibitor p18 - human
ALTERNATE_NAMES cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent
kinase CDK6 inhibitor p18
ORGANISM #formal_name Homo sapiens #common_name man
DATE 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
ACCESSIONS A55479
REFERENCE O'Keefe, C.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.;
#authors Guan, K.L.; Mattern, A.G.; Xiong, Y.
#journal Genes Dev. (1994) 8:2939-2952
#title Growth suppression by p18, a p16(INK4/MTS1)- and p14
(INK4B/MTS2)-related CDK6 inhibitor, correlates with
wild-type pRB function.
#cross-references MUID:95095079
#accession A55479
#molecule_type mRNA

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#residues 1-168 #label GUA
#cross-references GB:U17074; NID:G639713; PID:AA50074.1; PID:G639714
GENETICS
#gene GDB:CDKN2C
#map_position lp32-lp32
#cross-references GDB:594931
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology
cell cycle control; protein kinase inhibitor; tumor
suppressor
SUMMARY #length 168 #molecular-weight 18127 #checksum 9379

Query Match 25.5%; Score 249; DB 2; Length 168;
Best Local Similarity 39.0%; Pred. No. 1.74e-25;
Matches 46; Conservative 28; Mismatches 43; Indels 1; Gaps 1;

Db 6 GNELASAAAGDLEOLTSLQNNVNAONGFRTALQVMKLGNPETARLLRGANPDL 65
QY 14 SDEGLATPARGLVKVRHWEAGADPNVNRFGRRRAIQVMMGSRVAEALLLHGAEPNC 73
Db 66 KDRTGFA-VIHDAAAGFLDTLQTLLEFQADVNIENEGNLPHLAAKEGHLRVVEFL 122
QY 74 ADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAERGHDRVAGYL 131

RESULT 10
ENTRY #type complete
TITLE CDK4/CDK6 inhibitor p18 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
ACCESSIONS B57379
REFERENCE Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr,
#authors C.J.
#journal Mol. Cell. Biol. (1995) 15:2672-2681
#title Novel INK4 proteins, p19 and p18, are specific inhibitors of
the cyclin D-dependent kinases CDK4 and CDK6.
#cross-references MUID:95257948
#accession B57379
#status preliminary
#molecule_type mRNA
#residues 1-168 #label HIR
#cross-references GB:U19396; NID:G790566; PID:AA52193.1; PID:G790567
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology
cell cycle control
SUMMARY #length 168 #molecular-weight 18066 #checksum 8831

Query Match 25.3%; Score 247; DB 2; Length 168;
Best Local Similarity 38.2%; Pred. No. 3.99e-25;
Matches 47; Conservative 29; Mismatches 46; Indels 1; Gaps 1;

Db 6 GNELASAAAGDLEOLTSLQNNVNAONGFRTALQVMKLGNPETARLLRGANPDL 65
QY 14 SDEGLATPARGLVKVRHWEAGADPNVNRFGRRRAIQVMMGSRVAEALLLHGAEPNC 73
Db 66 KDRTGFA-VIHDAAAGFLDTLQTLLEFQADVNIENEGNLPHLAAKEGHLRVVEFL 124
QY 74 ADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAERGHDRVAGYL 133
Db 125 HTA 127
QY 134 ATG 136

RESULT 11
ENTRY #type complete
TITLE death-associated protein kinase (EC 2.7.1.-) - human
ALTERNATE_NAMES calmodulin-dependent protein kinase homolog; DAP kinase
ORGANISM #formal_name Homo sapiens #common_name man
DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
10-Jul-1998

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ACCESSIONS      I37275; S39269
REFERENCE        A55614
#authors        Deliss, L.P.; Feinstein, E.; Berissi, H.; Cohen, O.; Kimchi, A.
#journal         Genes Dev. (1995) 9:15-30
#title           Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell death.
#cross-references MUID:95129831
#accession       I37275
#molecule_type mRNA
#residues        1-1423 #label RES
#cross-references EMBL:X76104; NID:g434846; PID:g434847
GENETICS
#gene            GDB:DAPK1; DAPK
#map_position     9q34.1-9q34.1
#cross-references GDB:555932; OMIM:600831
FUNCTION
#description      catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate using ATP
#pathway          apoptosis
#note             activity is calmodulin dependent
CLASSIFICATION
#keywords         apoptosis; ATP; calmodulin binding; phosphotransferase; serine/threonine-specific protein kinase; tandem repeat
FEATURE
11-267           #domain protein kinase homology #label KIN
19-27            #region protein kinase ATP-binding motif
285-308          #region calmodulin binding status predicted
370-402          #domain ankyrin repeat homology #label AN1
403-435          #domain ankyrin repeat homology #label AN2
436-468          #domain ankyrin repeat homology #label AN3
470-502          #domain ankyrin repeat homology #label AN4
503-535          #domain ankyrin repeat homology #label AN5
536-568          #domain ankyrin repeat homology #label AN6
569-601          #domain ankyrin repeat homology #label AN7
602-634          #domain ankyrin repeat homology #label AN8
42,64,139,141   #active_site Lys, Glu, Asp, Lys #status predicted
SUMMARY          #length 1423 #molecular-weight 159161 #checksum 6280
Query Match      14.3%; Score 140; DB 1; Length 1423;
Best Local Similarity 32.2%; Pred. No. 4.79e-07;
Matches          37; Conservative 23; Mismatches 53; Indels 2; Gaps 2;
Db 509 LTASRGYHDIVCLAEHGDADNACDKGHIALHLYVRQMEYIKTLSSQGCFFDYQDR 568
QY 18 LATPARGLVKVRHSEAGADPNGVNRFRRAIQVMMGSGAR-VAELLHLLHGAEPNCADP 76
Db 569 HGNT-PLHVACKDGNMIPVALCEANCNLDISNKYGRTPPLHLAANGILDVRYL 622
QY 77 ATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAERGHDRDVAGYL 131
RESULT 12
ENTRY           B35049      #type complete
TITLE           ankyrin 1, erythrocyte splice form 3 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS        ankyrin 2.2, erythrocyte
ORGANISM        #formal_name Homo sapiens #common_name man
DATE            17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
ACCESSIONS      B35049
REFERENCE        Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.
#journal         Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
#title           CDNA sequence for human erythrocyte ankyrin.
#cross-references MUID:90175370
#accession       B35049
#status          preliminary
#molecule_type mRNA
#residues        1-1856 #label LAM

```

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GENETICS
#gene            GDB:ANK1; ANK
#map_position     8p11.2-8p11.2
#cross-references GDB:118737; OMIM:182900
CLASSIFICATION   #superfamily ankyrin; ankyrin repeat homology
KEYWORDS         alternative splicing
FEATURE
2-1856          #product ankyrin 1, erythrocyte form 3 #status predicted
                #label MAR
                #product ankyrin 2.2, erythrocyte #status predicted
                #label MA2
44-76           #domain ankyrin repeat homology #label ANO1
77-109          #domain ankyrin repeat homology #label ANO2
110-142         #domain ankyrin repeat homology #label ANO3
143-171         #domain ankyrin repeat homology #label ANO4
172-204         #domain ankyrin repeat homology #label ANO5
205-237         #domain ankyrin repeat homology #label ANO6
238-270         #domain ankyrin repeat homology #label ANO7
271-303         #domain ankyrin repeat homology #label ANO8
304-336         #domain ankyrin repeat homology #label ANO9
337-369         #domain ankyrin repeat homology #label AN10
370-402         #domain ankyrin repeat homology #label AN11
403-435         #domain ankyrin repeat homology #label AN12
436-468         #domain ankyrin repeat homology #label AN13
469-501         #domain ankyrin repeat homology #label AN14
502-534         #domain ankyrin repeat homology #label AN15
535-567         #domain ankyrin repeat homology #label AN16
568-600         #domain ankyrin repeat homology #label AN17
601-633         #domain ankyrin repeat homology #label AN18
634-666         #domain ankyrin repeat homology #label AN19
667-699         #domain ankyrin repeat homology #label AN20
700-732         #domain ankyrin repeat homology #label AN21
733-765         #domain ankyrin repeat homology #label AN22
766-798         #domain ankyrin repeat homology #label AN23
SUMMARY          #length 1856 #molecular-weight 203445 #checksum 6521
Query Match      14.3%; Score 140; DB 2; Length 1856;
Best Local Similarity 32.3%; Pred. No. 4.79e-07;
Matches          42; Conservative 25; Mismatches 55; Indels 8; Gaps 8;
Db 493 NAMPNLATTAG-HTPLHIAAREGHVETVLALLEKEASQACMTKGTPLHVAARYKVRV 551
QY 3 EENKMPGSGGSDEGLATPAR-GLVEKVRHSEAGADPNGVNRFRRAIQVMM-GSARV 60
Db 552 AELLERDAHPNAGKNLT-PLHVAHHNNLDIVKLLPRGGSP-HSP-AWNGYTPLHI 608
QY 61 AEILLHGAEPNCADPATLRPVHDAAREGFLDTL-VVLRHAGARLDVRDAG-GRLPVDL 118
Db 609 AAKONQVEVA 618
QY 119 AEERGHDRVA 128
RESULT 13
ENTRY           A35049      #type complete
TITLE           ankyrin 1, erythrocyte splice form 2 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS        ankyrin 2.2, erythrocyte
ORGANISM        #formal_name Homo sapiens #common_name man
DATE            27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
ACCESSIONS      A35049
REFERENCE        Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.
#journal         Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
#title           CDNA sequence for human erythrocyte ankyrin.
#cross-references MUID:90175370
#accession       A35049
#status          preliminary
#molecule_type mRNA
#residues        1-1880 #label LAM
#cross-references GB:M28880

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GENETICS
#gene GDB:ANK1; ANK
#cross-references GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS #alternative splicing; cytoskeleton
FEATURE
2-1880
#product ankyrin 1, erythrocyte form 2 #status predicted
#label MAT1
#product ankyrin 2.2, erythrocyte #status predicted
#label MA2
#domain ankyrin repeat homology #label AN01
#domain ankyrin repeat homology #label AN02
#domain ankyrin repeat homology #label AN03
#domain ankyrin repeat homology #label AN04
#domain ankyrin repeat homology #label AN05
#domain ankyrin repeat homology #label AN06
#domain ankyrin repeat homology #label AN07
#domain ankyrin repeat homology #label AN08
#domain ankyrin repeat homology #label AN09
#domain ankyrin repeat homology #label AN10
#domain ankyrin repeat homology #label AN11
#domain ankyrin repeat homology #label AN12
#domain ankyrin repeat homology #label AN13
#domain ankyrin repeat homology #label AN14
#domain ankyrin repeat homology #label AN15
#domain ankyrin repeat homology #label AN16
#domain ankyrin repeat homology #label AN17
#domain ankyrin repeat homology #label AN18
#domain ankyrin repeat homology #label AN19
#domain ankyrin repeat homology #label AN20
#domain ankyrin repeat homology #label AN21
#domain ankyrin repeat homology #label AN22
#domain ankyrin repeat homology #label AN23
#length 1880 #molecular-weight 206066 #checksum 6968

SUMMARY
Query Match 14.3%; Score 140; DB 2; Length 1880;
Best Local Similarity 32.3%; Pred. No. 4.79e-07;
Matches 42; Conservative 25; Mismatches 55; Indels 8; Gaps 8;

Db 493 NANPNLATAG-HTPLHIAAREGHVETVLLLEKASQACMTKGTPLTVAAYGKVRV 551
QY 3 ENKGMPSGGSGDEGLATPAR-GLVEKVRHSWEAGDPNGVNFERRAIQVMM-GSARV 60

Db 552 AELLERDAPNAKNGKIT-PLHVAVHNNLDIVKLLPRGGSP-HSP-AWNGYTPLHI 608
QY 61 AELLHLGAEPNCADPATLTPVDAARSGFDTL-VLHRAGAKLDVRDAW-GRLPVDL 118

Db 609 AAKQNOVEVA 618
QY 119 AEERGHDRVA 128

RESULT 14
ENTRY SUHUK #type complete
TITLE ankyrin 1, erythrocyte splice form 1 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS ankyrin 2.2
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
22-Jun-1999

ACCESSIONS S08275; A33219; PC2220; A35443
REFERENCE S08275
#authors Lux, S.E.; John, K.M.; Bennett, V.
#journal Nature (1990) 344:36-42
#title Analysis of cDNA for human erythrocyte ankyrin indicates a
repeated structure with homology to tissue-differentiation
and cell-cycle control proteins.
#cross-references MUID:90158830
#accession S08275
#molecule_type mRNA
#residues 1-1881 #label LUL1
#cross-references EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702

#accession A33219
#molecule_type protein
#residues 2-7,'X',9-17,'X',19-20,'T',22-30:733-749,'A',751-753;
828-833,'X',835-855,'X',857-859,'XX',862-871;959-1003;
1106-1120,'XX',1123-1128;1149-1172:1282-1285,'P',
1287-1288;1307-1332:1345-1365,'X',1367:1383-1427;
1601-1630:1686-1698,'D',1700;1763-1772 #label L0X
#note 845-Arg and 1392-Thr were also found
REFERENCE PC2220
#authors Hermann, J.; Barel, M.; Frade, R.
#journal Biochem. Biophys. Res. Commun. (1994) 204:453-460
#title Human erythrocyte ankyrin, a cytoskeleton component,
generates the p57 membrane proteinase which cleaves C3, the
third component of complement.
#cross-references MUID:95071348
#accession PC2220
#molecule_type protein
#residues 910-929 #label HER
REFERENCE A35443
#authors Davis, L.H.; Bennett, V.
#journal J. Biol. Chem. (1990) 265:10589-10596
#title Mapping the binding sites of human erythrocyte ankyrin for
the anion exchanger and spectrin.
#cross-references MUID:90285190
#accession A35443
#molecule_type protein
#residues 'X',5,'X',7-12:403-417,'X',419-422,'H',424,'LQ',797-800,
'L',802-814;862-863,'X',865-877,'X',899-901,'T',
903-909,'X',911-912 #label DAV

GENETICS
#gene GDB:ANK1; ANK
#cross-references GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS #alternative splicing; phosphoprotein
FEATURE
2-1881
#product ankyrin 1, erythrocyte form 1 #status predicted
#label MAT1
#product ankyrin 2.2, erythrocyte #status predicted
#label MAT2
#domain 89K #status predicted #label DOM1
#region anion exchange protein binding
#domain ankyrin repeat homology #label AN01
#domain ankyrin repeat homology #label AN02
#domain ankyrin repeat homology #label AN03
#domain ankyrin repeat homology #label AN04
#domain ankyrin repeat homology #label AN05
#domain ankyrin repeat homology #label AN06
#domain ankyrin repeat homology #label AN07
#domain ankyrin repeat homology #label AN08
#domain ankyrin repeat homology #label AN09
#domain ankyrin repeat homology #label AN10
#domain ankyrin repeat homology #label AN11
#domain ankyrin repeat homology #label AN12
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#domain ankyrin repeat homology #label AN16
#domain ankyrin repeat homology #label AN17
#domain ankyrin repeat homology #label AN18
#domain ankyrin repeat homology #label AN19
#domain ankyrin repeat homology #label AN20
#domain ankyrin repeat homology #label AN21
#domain ankyrin repeat homology #label AN22
#domain 62K #status predicted #label DOM2
#region spectrin binding
#domain 55K #status predicted 206275 #checksum 2619
SUMMARY
Query Match 14.3%; Score 140; DB 1; Length 1881;
Best Local Similarity 32.3%; Pred. No. 4.79e-07;
Matches 42; Conservative 25; Mismatches 55; Indels 8; Gaps 8;

```

```

Db 493 NANPLATTAG-HTPLHTAAREGHVETVLALLEKEASQACMTKGFPLHVAAKYKVRV 551
Qy 3 EENKMPGGSGDEGLATPAR-GLYKVRHSWEAGDPNGVNRFGRRAIQVMM-GSARV 60
      |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 552 AELLERDAHPNAGKNGLT-PLHAVAHNNLDIVKLLPRGGSP-HSP-AWNGYTPLHI 608
Qy 61 AELLLLHGAEPNCADPATLTPRVHDAAREGFDTL-VVLRAGARLDVRDAW-GRLPVDL 118
      |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 609 AAKQNQVEVA 618
Qy 119 AEERGHDRVA 128

RESULT 15
ENTRY S37771 #type complete
TITLE ankyrin, erythrocyte - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 27-May-1994 #sequence_revision 03-Aug-1995 #text_change
13-Aug-1999
ACCESSIONS S37771
REFERENCE S37771
#authors Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.;
Lux, S.E.; Barker, J.E.
#journal J. Biol. Chem. (1993) 268:9533-9540
#title Complex patterns of sequence variation and multiple 5' and 3'
ends are found among transcripts of the erythroid ankyrin
gene.
#cross-references MUID:93252825
#accession S37771
#status preliminary
#molecule_type mRNA
#residues 1-1848 #label BIR
#cross-references EMBL:X69063; NID:g311816; PIDN:CAA48801.1;
PID:g311817
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS alternative splicing
FEATURE
48-80 #domain ankyrin repeat homology #label AN01\
81-113 #domain ankyrin repeat homology #label AN02\
114-146 #domain ankyrin repeat homology #label AN03\
147-175 #domain ankyrin repeat homology #label AN04\
176-208 #domain ankyrin repeat homology #label AN05\
209-241 #domain ankyrin repeat homology #label AN06\
242-274 #domain ankyrin repeat homology #label AN07\
275-307 #domain ankyrin repeat homology #label AN08\
308-340 #domain ankyrin repeat homology #label AN09\
341-373 #domain ankyrin repeat homology #label AN10\
374-406 #domain ankyrin repeat homology #label AN11\
407-439 #domain ankyrin repeat homology #label AN12\
440-472 #domain ankyrin repeat homology #label AN13\
473-505 #domain ankyrin repeat homology #label AN14\
506-538 #domain ankyrin repeat homology #label AN15\
539-571 #domain ankyrin repeat homology #label AN16\
572-604 #domain ankyrin repeat homology #label AN17\
605-637 #domain ankyrin repeat homology #label AN18\
638-670 #domain ankyrin repeat homology #label AN19\
671-703 #domain ankyrin repeat homology #label AN20\
704-736 #domain ankyrin repeat homology #label AN21\
737-769 #domain ankyrin repeat homology #label AN22\
770-802 #domain ankyrin repeat homology #label AN23\
SUMMARY #length 1848 #molecular-weight 202576 #checksum 2542

Query Match 14.0%; Score 137; DB 2; Length 1848;
Best Local Similarity 33.9%; Pred. No. 1.38e-06;
Matches 39; Conservative 21; Mismatches 48; Indels 7; Gaps 7;

Db 511 LHTAAREGHVDTALLLEKEASQACMTKGFPLHVAAKYKVRVLAELLLEHDAHNPAG 570
Qy 18 LATPAR-GLYKVRHSWEAGDPNGVNRFGRRAIQVMM-GSARVAELLLLHGAEPNCAD 75
      |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 571 KNGLT-PLHAVAHNNLDIVKLLPRGGSP-HSP-AWNGYTPLHTAAKQNQVEVA 622
      |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
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Qy 76 PATLRPVHDAAREGFDTL-VVLRAGARLDVRDAW-GRLPVDLAERGHDRVA 128

Search completed: Thu Jul 20 08:38:48 2000

Job time : 13 secs.

(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:39:06 2000; MasPar time 6.93 Seconds
Tabular output not generated. 602.124 Million cell updates/sec

Title: >US-09-016-869A-4
Description: (1-137) from US09016869A.pep
Perfect Score: 977
Sequence: 1 MREENKMGSGGSDEGLAT.....LAERGHVDVAGYLRTATGD 137

Scoring table: PAM 150
Gap 11

Searched: 83857 segs, 30454973 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 43.541; Variance 77.735; scale 0.560

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB	ID	Description	Pred. No.
1	919	94.1	138	1	CDN5_HUMAN	CYCLIN-DEPENDENT KINAS	7.32e-179
2	751	76.9	130	1	CDN5_RAT	CYCLIN-DEPENDENT KINAS	4.85e-140
3	749	76.7	130	1	CDN5_MOUSE	CYCLIN-DEPENDENT KINAS	1.40e-139
4	692	70.8	136	1	CDN2_HUMAN	CYCLIN-DEPENDENT KINAS	1.62e-126
5	581	59.5	167	1	CDN2_MOUSE	CYCLIN-DEPENDENT KINAS	2.75e-101
6	572	58.5	171	1	CDN2_MONDO	CYCLIN-DEPENDENT KINAS	2.96e-99
7	329	33.7	166	1	CDN7_HUMAN	CYCLIN-DEPENDENT KINAS	9.77e-46
8	315	32.2	166	1	CDN7_MOUSE	CYCLIN-DEPENDENT KINAS	9.05e-43
9	249	25.5	168	1	CDN6_HUMAN	CYCLIN-DEPENDENT KINAS	4.38e-29
10	247	25.3	168	1	CDN6_MOUSE	CYCLIN-DEPENDENT KINAS	1.11e-28
11	140	14.3	1431	1	DAPK_HUMAN	DEATH-ASSOCIATED PROTE	2.39e-08
12	140	14.3	1880	1	ANK1_HUMAN	ANKYRIN R (ANKYRINS 2.	2.39e-08
13	137	14.0	1862	1	ANK1_MOUSE	ANKYRIN.	7.81e-08
14	133	13.6	2524	1	NOTC_XENLA	NEUROGENIC LOCUS NOTCH	3.72e-07
15	131	13.4	1839	1	ANKB_HUMAN	ANKYRIN, BRAIN VARIANT	8.05e-07
16	131	13.4	3924	1	ANKB_MOUSE	ANKYRIN, BRAIN VARIANT	8.05e-07
17	130	13.3	2531	1	NTC1_RAT	NEUROGENIC LOCUS NOTCH	1.18e-06
18	129	13.2	2318	1	NTC3_MOUSE	NEUROGENIC LOCUS NOTCH	1.73e-06
19	129	13.2	2444	1	NTC1_HUMAN	NEUROGENIC LOCUS NOTCH	1.73e-06
20	128	13.1	2437	1	NOTC_BRARE	NEUROGENIC LOCUS NOTCH	2.54e-06
21	125	12.8	2531	1	NTC1_MOUSE	NEUROGENIC LOCUS NOTCH	7.91e-06
22	122	12.5	677	1	SKD3_MOUSE	SKD3 PROTEIN.	2.43e-05
23	121	12.4	2703	1	NOTC_DROME	NEUROGENIC LOCUS NOTCH	3.53e-05

24	118	12.1	323	1	ANKH_CHRVI	ANKYRIN HOMOLOG PRECUR	1.07e-04
25	115	11.8	1964	1	NTC4_MOUSE	NEUROGENIC LOCUS NOTCH	3.18e-04
26	108	11.1	248	1	FNRL_RHOSH	TRANSSCRIPTIONAL ACTIVA	3.82e-03
27	108	11.1	446	1	BCL3_HUMAN	B-CELL LYMPHOMA 3-ENCO	3.82e-03
28	103	10.5	679	1	RNSA_MOUSE	2-5A-DEPENDENT RIBONUC	2.13e-02
29	103	10.5	971	1	KBFL_MOUSE	NUCLEAR FACTOR NF-KAPP	2.13e-02
30	102	10.4	740	1	Y050_HUMAN	HYPOPHETICAL PROTEIN K	2.99e-02
31	100	10.2	227	1	PHLB_SERLI	PHLB PROTEIN PRECURSOR	5.85e-02
32	100	10.2	341	1	YGLI_STRCO	HYPOTHETICAL PROTEIN I	5.85e-02
33	99	10.1	1295	1	GLP1_CAEEL	GLP-1 PROTEIN PRECURSO	8.15e-02
34	98	10.0	182	1	SRPB_SYN7	SRPB PROTEIN.	1.13e-01
35	98	10.0	414	1	GABD_MOUSE	GA BINDING PROTEIN BET	1.13e-01
36	98	10.0	500	1	CACD_DROME	DEVELOPMENTAL PROTEIN	1.13e-01
37	98	10.0	571	1	GLS1_CAEEL	POTATIVE GLUTAMINASE D	1.13e-01
38	98	10.0	785	1	SYFB_THETH	PHENYLALANYL-TRNA SYNT	1.13e-01
39	97	9.9	347	1	GABC_HUMAN	GA BINDING PROTEIN BET	1.57e-01
40	97	9.9	347	1	GABC_MOUSE	GA BINDING PROTEIN BET	1.57e-01
41	97	9.9	382	1	GABB_MOUSE	GA BINDING PROTEIN BET	1.57e-01
42	97	9.9	383	1	GABB_HUMAN	GA BINDING PROTEIN BET	1.57e-01
43	97	9.9	545	1	TCPA_SCHMA	T-COMPLEX PROTEIN 1, A	1.57e-01
44	97	9.9	937	1	YKRI_CAEEL	HYPOTHETICAL 112.1 KD	1.57e-01
45	96	9.8	1401	1	LATA_LATMA	ALPHA-LATROTOXIN PRECU	2.17e-01

ALIGNMENTS

RESULT 1
ID CDN5_HUMAN STANDARD; PRT; 138 AA.
AC P42772;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
DE (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).
GN CDKN2B OR MTS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95095079.
RA Guan K.-L., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
RA Matera G.A., Xiong Y.;
RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related
RT CDK6 inhibitor, correlates with wild-type pRB function.";
RL Genes Dev. 8:2939-2952(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94359613.
RA Hannon G.J., Beach D.;
RT "p15INK4B is a potential effector of TGF-beta-induced cell cycle
RT arrest.";
RL Nature 371:257-261(1994).
RN [3]
RP SEQUENCE OF 53-138 FROM N.A.
RX MEDLINE; 94204645.
RA Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
RA Skolnick M.H.;
RT "A cell cycle regulator potentially involved in genesis of many tumor
RT types.";
RL Science 264:436-440(1994).
RN [4]
RP VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.
RX MEDLINE; 95186190.
RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zarwala M.,
RA Xiong Y., Beach D.H., Yokota J., Harris C.C.;
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
RT primary and metastatic lung cancer.";
RL Cancer Res. 55:1448-1451(1995).
CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -!- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.


```

RC STRAIN=C57BL/6J X DBA;
RX MEDLINE; 9732242.
RA Malumbres M., de Castro I., Santos J., Melendez B., Mangués R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RT "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by
RT deletion and de novo methylation with independence of p16INK4a
RT alterations in murine primary T-cell lymphomas.";
RL Oncogene 14:1361-1370(1997)
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -1- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
CC -1- INDUCTION: BY TGF-BETA.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC -----
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CC -----
DR EMBL; U66085; AAB39833.1; -.
DR EMBL; U66084; AAB39833.1; JOINED.
DR MGD; MGI:104737; CDKN2B.
DR PFAM; PF00023; ank; 3.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.
FT DOMAIN 5 95 2 X ANK MOTIF REPEATS.
FT REPEAT 5 31 ANK MOTIF 1 (INCOMPLETE).
FT REPEAT 65 95 ANK MOTIF 2.
SQ SEQUENCE 130 AA; 13788 MW; 7AAD60FF52ECFF9 CRC64;
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Query Match 76 78; Score 749; DB 1; Length 130;
Best Local Similarity 85.28; Pred. No. 1.40e-139;
Matches 109; Conservative 11; Mismatches 7; Indels 1; Gaps 1;
Db 3 GGSDDAGLATAARGQVETVRLLEAGADPNALNRRFRRTIQVNMGSAQVAELLLHGA 62
QY 11 GGSDEGLATPA-RGLVEKVRHSWEACADPNVNRFRGRRAIQVNMGSAQVAELLLHGA 69
Db 63 EPCNADPATITRPVHDAAEGFLDTLVLRHAGARLDVCDAGRLPVDLAEQGHRIAR 122
QY 70 EPCNADPATITRPVHDAAEGFLDTLVLRHAGARLDVCDAGRLPVDLAEQGHRIAR 129
Db 123 YLHAATGD 130
QY 130 YLRTATGD 137
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RESULT 4
ID CDN2_HUMAN STANDARD; PRT; 156 AA.
AC P42771; Q15191;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A)
DE (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1).
GN CDKN2A OR CDKN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 94081956.
RA Serrano M., Hannon G.J., Beach D.;
RT "A new regulatory motif in cell-cycle control causing specific
RT inhibition of cyclin D/CDK4.";
RL Nature 366:704-707(1993).
RN [2]

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RP SEQUENCE OF 51-152 FROM N.A.
RX MEDLINE; 94204645.
RA Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
RA Skolnick M.H.;
RT "A cell cycle regulator potentially involved in genesis of many tumor
RT types.";
RL Science 264:436-440(1994).
RN [3]
RP SEQUENCE OF 1-20 FROM N.A.
RX MEDLINE; 96182088.
RA Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;
RT "Regulation of p16CDKN2 expression and its implications for cell
RT immortalization and senescence.";
RL Mol. Cell. Biol. 16:859-867(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.
RX MEDLINE; 98421670.
RA Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;
RT "Structural basis for inhibition of the cyclin-dependent kinase Cdk6
RT by the tumour suppressor p16INK4a.";
RL Nature 395:237-243(1998).
RN [5]
RP REVIEW ON MELANOMA VARIANTS.
RX MEDLINE; 96377761.
RA Dracopoli N.C., Fountain J.W.;
RT "CDKN2 mutations in melanoma.";
RL Cancer Surv. 26:115-132(1996).
RN [6]
RP REVIEW ON VARIANTS.
RX MEDLINE; 96303699.
RA Smith-Soerensen B., Hovig E.;
RT "CDKN2A (p16INK4A) somatic and germline mutations.";
RL Hum. Mutat. 7:294-303(1996).
RN [7]
RP VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).
RX MEDLINE; 94338359.
RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41
RT (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small
RT cell lung carcinomas.";
RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).
RN [8]
RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.
RX MEDLINE; 95078916.
RA Hussusan C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,
RA Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;
RT "Germline p16 mutations in familial melanoma.";
RL Nat. Genet. 8:15-21(1994).
RN [9]
RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.
RX MEDLINE; 95060835.
RA Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
RA Abraham J.M., Meltzer S.J.;
RT "The MTS1 gene is frequently mutated in primary human esophageal
RT tumors.";
RL Oncogene 9:3737-3741(1994).
RN [10]
RP VARIANTS.
RX MEDLINE; 95188190.
RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,
RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
RT primary and metastatic lung cancer.";
RL Cancer Res. 55:1448-1451(1995).
RN [11]
RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.
RX MEDLINE; 96121580.
RA Walker G.J., Hussusan C.J., Flores J.F., Glendening J.M.,
RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;
RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma
RT kindreds.";

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RL Hum. Mol. Genet. 4:1845-1852(1995).
 RN [12]
 RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
 RX MEDLINE; 95375774.
 RA Ranade K., Hussussian C.J., Sikorski R.S., Varnus H.E., Beach D.,
 RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,
 RA Dracopoli N.C.;
 RA "Mutations associated with familial melanoma impair p16INK4
 RT function.";
 RT Nat. Genet. 10:114-116(1995).
 RL [13]
 RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.
 RX MEDLINE; 96323259.
 RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
 RA Luchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,
 RA Isselbacher K.J., Sober A.J., Haber D.A.;
 RT "Prevalence of germline mutations in p16, p19ARF, and CDK4 in
 RT familial melanoma: analysis of a clinic-based population.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).
 RL [14]
 RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.
 RX MEDLINE; 97472457.
 RA Harland M., Meloni R., Gruls N., Pinney E., Brookes S., Spurr N.K.,
 RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,
 RA Bishop D.T., Bishop J.N.;
 RT "Germline mutations of the CDKN2 gene in UK melanoma families.";
 RL Hum. Mol. Genet. 6:2061-2067(1997).
 RL [15]
 RP VARIANTS FAMILIAL MELANOMA.
 RX MEDLINE; 98087572.
 RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
 RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Pallierets B.;
 RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone
 RT families in France.";
 RL Hum. Mol. Genet. 7:209-216(1998).
 RL [16]
 RP VARIANTS PANCREATIC CARCINOMA CYS-146.
 RX MEDLINE; 98087572.
 RA Moskaluk C.A., Hruban R.H., Lieman A., Smyrk T., Fusaro L.,
 RA Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;
 RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple
 RT pancreatic carcinomas.";
 RL Hum. Mutat. 12:70-70(1998).
 RL [18]
 RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.
 RA Gretarsdottir S., Olafsdottir G.H., Borg A.;
 RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,
 RT glioma and carcinoma of the pancreas.";
 RL Hum. Mutat. 12:212-212(1998).
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS
 CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
 CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.
 CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
 CC -1- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A
 CC WIDE RANGE OF TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
 CC INHIBITORS.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
 CC -----
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 CC -----
 DR EMBL; L27211; AAA92554.1; -;
 DR EMBL; U12820; AAB60645.1; -;

DR EMBL; U12818; AAB60645.1; JOINED.
 DR EMBL; U12819; AAB60645.1; JOINED.
 DR EMBL; S69804; AAD14048.1; -;
 DR EMBL; X94154; CAA63870.1; -;
 DR PDB; 1BI7; 16-FEB-99.
 DR MIN; 600160; -;
 DR PFAM; PF00023; ank; 3.
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;
 KW Polymorphism; 3D-structure.
 FT DOMAIN 12 141
 FT REPEAT 12 43
 FT REPEAT 44 75
 FT REPEAT 77 109
 FT REPEAT 110 141
 FT REPEAT 14 14
 FT VARIANT 16 16
 FT VARIANT 20 20
 FT VARIANT 20 20
 FT VARIANT 23 23
 FT VARIANT 24 24
 FT VARIANT 24 24
 FT VARIANT 26 26
 FT VARIANT 32 32
 FT VARIANT 33 33
 ... Note: remainder of annotations omitted.
 Query Match 70.8%; Score 692; DB 1; Length 156;
 Best Local Similarity 85.8%; Pred. No. 1.62e-126;
 Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
 Db 16 LATAAARGVEEVRLLEAGALPNAPNSYGRPRPQVMGMSARVAELLLHGAENPCADP 75
 Qy 18 LATPA-RGLVEKVRHSWEGADPNVGRRAQVMGMSARVAELLLHGAENPCADP 76
 Db 76 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLAELGHRDVARVYLRAGA 135
 Qy 77 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLAELGHRDVARVYLRAGA 136
 RESULT 5
 ID CDN2_MOUSE STANDARD; PRT; 167 AA.
 AC P51480;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A).
 GN CDKN2A OR P16INK4A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 95380169.
 RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
 RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
 RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
 RL Oncogene 11:635-645(1995).
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
 CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
 CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE
 CC PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.

CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES
CC CONTAINED CDK6.
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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CC
CC EMBL; L76150; AAA85453.1; -;
CC MGD; MGI:104738; CDKN2A.
CC PFAM; PF00023; ank; 2.
CC Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CC DOMAIN 4 152 4 X ANK MOTIF REPEATS.
CC REPEAT 4 34 ANK MOTIF 1 (INCOMPLETE).
CC REPEAT 35 66 ANK MOTIF 2.
CC REPEAT 68 100 ANK MOTIF 3.
CC REPEAT 101 152 ANK MOTIF 4.
CC VARSPLIC 1 42 MISSING (IN SHORT ISOFORM).
CC SEQUENCE 167 AA; 17870 MW; 88C4588A105ECB8F CRC64;
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CC Query Match 59.5%; Score 581; DB 1; Length 167;
CC Best Local Similarity 65.6%; Pred. No. 2,75e-101;
CC Matches 80; Conservative 20; Mismatches 22; Indels 0; Gaps 0;
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CC Db 3 SAADRLARAAGRVHDVRLALLEGVSPNAPNSFGRTPIQVMMGNVHVAALLNLTGADSN 62
CC Qy 13 GSDEGLATPARGLVKVEKSHSWEAGADPNVNRFGRRAIQVMMGSGARVAELLHLGAEPN 72
CC
CC Db 63 CEDPTFSRPVHDAAREGFLDTLVVHSGARLDVRDAGRLPDLAERGHQDIVRLR 122
CC Qy 73 CADPATLTPRVHDAAREGFLDTLVVHHRAGARLDVRDAGRLPVDLAERGRDVGAYLR 132
CC
CC Db 123 SA 124
CC Qy 133 TA 134
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CC RESULT 6
CC ID CDN2_MONDO STANDARD; PRT; 171 AA.
CC AC 077617;
CC DT 15-JUL-1999 (Rel. 38, Created)
CC DT 15-JUL-1999 (Rel. 38, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A)
CC DE (TUMOR SUPPRESSOR CDKN2A).
CC GN CDKN2A.
CC OS Monodelphis domestica (Short-tailed grey opossum).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC OC Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
CC [1]
CC RP SEQUENCE FROM N.A.
CC RA Sherburn T.E., Gale J.M., Ley R.D.;
CC RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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CC
CC EMBL; AF064808; AAC23669.1; -;
CC DR EMBL; AF064808; AAC23670.1; -;
CC DR PFAM; PF00023; ank; 3.
CC Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CC DOMAIN 46 169 4 X ANK MOTIF REPEATS.
CC REPEAT 46 77 ANK MOTIF 1 (INCOMPLETE).
CC REPEAT 78 109 ANK MOTIF 2.
CC REPEAT 111 143 ANK MOTIF 3.
CC REPEAT 144 169 ANK MOTIF 4.
CC VARSPLIC 1 34 MISSING (IN SHORT ISOFORM).
CC SEQUENCE 171 AA; 18707 MW; 694264F5D0F4F6CC CRC64;
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CC Query Match 58.5%; Score 572; DB 1; Length 171;
CC Best Local Similarity 69.2%; Pred. No. 2.96e-99;
CC Matches 83; Conservative 17; Mismatches 19; Indels 1; Gaps 1;
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CC Db 46 SGEKLTEAARGTEVTVTELELGTNPNAVNRFGRSALQVMMGNVRLAAILQYGAEPN 105
CC Qy 14 SDEGLA-TPARGLVKVEKSHSWEAGADPNVNRFGRRAIQVMMGSGARVAELLHLGAEPN 72
CC
CC Db 106 TPDPTTLTPVHDAAREGFLDTLMLHHRAGARLDVRDAGRLPVDLAEEQGHLLVAYLR 165
CC Qy 73 CADPATLTPRVHDAAREGFLDTLVVHHRAGARLDVRDAGRLPVDLAERGRDVGAYLR 132
CC
CC RESULT 7
CC ID CDN7_HUMAN STANDARD; PRT; 166 AA.
CC AC P55273; Q13102;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 01-JUL-1999 (Rel. 38, Last annotation update)
CC DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
CC GN CDKN2D.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE-BONE MARROW;
CC RX MEDLINE; 96121373.
CC RA Okuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J.,
CC Lahti J.M., Sherr C.J., Downing J.R.;
CC RT "Molecular cloning, expression pattern, and chromosomal localization
CC of human CDKN2D/INK4d, an inhibitor of cyclin D-dependent kinases.";
CC RL Genomics 29:623-630(1995).
CC [2]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE; 96362662.
CC RA Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,
CC Zariwala M., Madera A.G., Xiong Y.;
CC RT "Isolation and characterization of p19INK4d, a p16-related inhibitor
CC specific to CDK6 and CDK4.";
CC RL Mol. Biol. Cell 7:57-70(1996).
CC [3]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE-THYMUS;
CC RX MEDLINE; 95257949.
CC RA Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.;
CC RT "Identification of human and mouse p19, a novel CDK4 and CDK6
CC inhibitor with homology to p16ink4.";
CC RL Mol. Cell. Biol. 15:2682-2688(1995).
CC [4]
CC RP SEQUENCE FROM N.A.
CC RA Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,
CC Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
CC Bishop D.T.;
CC RT "Mutation testing in melanoma families: INK4A, CDK4 and INK4D.";

RN SEQUENCE FROM N.A.
 RX MEDLINE; 95095079.
 RA Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
 RA Matera G.A., Xiong Y.;
 RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related
 RT CDK6 inhibitor, correlates with wild-type pRB function.";
 RL Genes Dev. 8:2939-2952(1994).
 RN [2]
 RN SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72.
 RP TISSUE-BREAST;
 RC MEDLINE; 98300299.
 RX Blais A., Labrie Y., Pouliot F., Lachance Y., Labrie C.;
 RA "Structure of the gene encoding the human cyclin-dependent kinase
 RT inhibitor p18 and mutational analysis in breast cancer.";
 RL Biochem. Biophys. Res. Commun. 247:146-153(1998).
 RN [3]
 RN VARIANT BREAST CANCER PRO-72.
 RP MEDLINE; 96438606.
 RX Lapointe J., Lachance Y., Labrie Y., Labrie C.;
 RA "A p18 mutant defective in CDK6 binding in human breast cancer
 RT cells.";
 RL Cancer Res. 56:4586-4589(1996).
 RN [4]
 RN X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
 RP MEDLINE; 98100086.
 RA Venkataramani R., Swaminathan K., Marmorstein R.;
 RT "Crystal structure of the CDK4/6 inhibitory protein p18INK4c provides
 RT insights into ankyrin-like repeat structure/function and
 RT tumor-derived p16INK4 mutations.";
 RL Nat. Struct. Biol. 5:74-81(1998).
 RN [5]
 RN STRUCTURE BY NMR.
 RP MEDLINE; 99175088.
 RA Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Maille P., Selby T.,
 RA Tsai M.-D.;
 RT "Tumor suppressor INK4: determination of the solution structure of
 RT p18INK4c and demonstration of the functional significance of loops in
 RT p18INK4c and p16INK4A.";
 RL Biochemistry 38:2930-2940(1999).
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
 CC CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
 CC ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
 CC -1- SUBUNIT: HETERODIMER OF P18 WITH CDK6.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SKELETAL MUSCLE. ALSO
 CC FOUND IN PANCREAS AND HEART.
 CC -1- DISEASE: CDKN2C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
 CC INHIBITORS.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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 CC EMBL: U17074; AAC50074.1; --
 CC EMBL: AF041248; AAC39782.1; --
 CC EMBL: AF041250; AAC39783.1; --
 CC EMBL: AF041249; AAC39783.1; JOINED.
 CC PDB: 1IIB; 13-JAN-99.
 CC PDB: 1BU9; PRELIMINARY.
 CC MIM: 603369; --
 CC PFAM: PF00023; ank; 3.
 CC Cell cycle; Repeat; ANK repeat; Disease mutation; 3D-structure.
 CC DOMAIN 5 135 4 X ANK MOTIF REPEATS.
 CC FT REPEAT 5 36 ANK MOTIF 1.
 CC FT REPEAT 37 68 ANK MOTIF 2.
 CC FT REPEAT 69 101 ANK MOTIF 3.
 CC FT REPEAT 102 135 ANK MOTIF 4.
 CC

FT VARIANT 72 72 A -> P (IN BREAST CANCER; LOSS OF CDK6
 FT INTERACTION).
 FT /FTIQ-VAR_001490.
 SQ SEQUENCE 168 AA; 18127 MW; 5D66AFA715186E9A CRC64;
 Query Match 25.5%; Score 249; DB 1; Length 168;
 Best Local Similarity 39.08; Pred. No. 4.38e-29; Indels 1; Gaps 1;
 Matches 46; Conservative 28; Mismatches 43;
 DB 6 GNELASAAAARGDLEQLTSLQNNVNVNAQNGFGRTALQVNMKGNPETARLLRLLRGNPDL 65
 QY 14 SDGLATPARGLVEKVRHSHWEACADPNVNFGRRAIQVMMGSGARVAELLHLHGAEPNC 73
 DB 66 KRTGFA-VIHDAARAGFDLTLOTLLFQADVNINENEGNPLHLAAKEGHLRVFEL 122
 QY 74 ADPATLTPVHDAAREGFDLTLLVLRHAGARLDVRDANGRLPVDLAERGRDVGVL 131
 RESULT 10
 ID CDN6_MOUSE STANDARD; PRT; 168 AA.
 AC Q60772;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
 DE KINASE 4 INHIBITOR C) (P18-INK4C).
 GN CDKN2C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL KAPLAN;
 RX MEDLINE; 95257948.
 RA Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
 RT "Novel INK4 proteins, p19 and p18, are specific inhibitors of the
 RT cyclin D-dependent kinases CDK4 and CDK6.";
 RL Mol. Cell. Biol. 15:2672-2681(1995).
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
 CC CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
 CC ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
 CC -1- SUBUNIT: HETERODIMER OF P18 WITH CDK6 (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
 CC INHIBITORS.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U19596; AAC52193.1; --
 CC MGD; MGI:105388; CDKN2C.
 CC PFAM: PF00023; ank; 3.
 CC Cell cycle; Repeat; ANK repeat.
 CC DOMAIN 5 135 4 X ANK MOTIF REPEATS.
 CC FT REPEAT 5 36 ANK MOTIF 1.
 CC FT REPEAT 37 68 ANK MOTIF 2.
 CC FT REPEAT 69 101 ANK MOTIF 3.
 CC FT REPEAT 102 135 ANK MOTIF 4.
 SQ SEQUENCE 168 AA; 18056 MW; BC8D5489307E128 CRC64;
 Query Match 25.3%; Score 247; DB 1; Length 168;
 Best Local Similarity 38.2%; Pred. No. 1.11e-28; Indels 1; Gaps 1;
 Matches 47; Conservative 29; Mismatches 46;
 DB 6 GNELASAAAARGDLEQLTSLQNNVNVNAQNGFGRTALQVNMKGNPETARLLRLLRGNPDL 65
 QY 14 SDGLATPARGLVEKVRHSHWEACADPNVNFGRRAIQVMMGSGARVAELLHLHGAEPNC 73

Db 66 KDTGFA-VIHDARAGFLDTVQALLERQADVNTEDNEGNLPLHLAAKEGLHPVVEFLMK 124
| : : : : : | | | | | : : : : : | | | | | : : : : : |
Qy 74 ADPATLTPRVHDAAREGEFLDTLVVHLRAGARLDVRDANGRLPVDLAERGRHVDVAGYLRT 133
| : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 125 HTA 127
| : : : : : | | | | | : : : : : | | | | | : : : : : |
Qy 134 ATG 136
| : : : : : | | | | | : : : : : | | | | | : : : : : |
RESULT 11
ID DAPK_HUMAN STANDARD; PRT; 1431 AA.
AC P53355;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
GN DAPK1 OR DAPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95129831.
RA Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
RT "Identification of a novel serine/threonine kinase and a novel 15-kD
protein as potential mediators of the gamma interferon-induced cell
death.";
RL Genes Dev. 9:15-30(1995).
RN [2]
RP REVISIONS TO 164-171.
RA Feinstein E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
DEATH.
CC -1- PTM: AUTOPHOSPHORYLATED.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 8 ANK REPEATS.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X76104; CAA53712.1; -;
DR HSP; Q63450; 1A06.
DR MIM; 600831; -;
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PFAM; PF00023; ank; 8.
DR PFAM; PF00069; pkinase; 1.
DR PFAM; PF00531; death; 1.
DR Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
KW phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
FT DOMAIN 13 266 PROTEIN KINASE
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT DOMAIN 267 334 CALMODULIN-BINDING.
FT DOMAIN 373 637 8 X ANK MOTIF REPEATS.
FT REPEAT 373 405 ANK MOTIF 1.
FT REPEAT 406 438 ANK MOTIF 2.
FT REPEAT 439 471 ANK MOTIF 3.
FT REPEAT 473 505 ANK MOTIF 4.
FT REPEAT 506 538 ANK MOTIF 5.
FT REPEAT 539 571 ANK MOTIF 6.
FT REPEAT 572 604 ANK MOTIF 7.
FT REPEAT 605 637 ANK MOTIF 8.

FT DOMAIN 1313 1397 DEATH DOMAIN.
FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.
SQ SEQUENCE 1431 AA; 160017 MW; 9EB84811004A155B CRC64;
Query Match 14.3%; Score 140; DB 1; Length 1431;
Best Local Similarity 32.2%; Pred. No. 2.39e-08;
Matches 37; Conservative 23; Mismatches 53; Indels 2; Gaps 2;
Db 517 LTASARGYHDIVCELAEGHAGDLNACDKDGHIALHAYRRCOMIEYIKTLISQCGFVYQDR 576
| : : : : : | | | | | : : : : : | | | | | : : : : : |
Qy 18 LATPARGLVKEVYRHSWEAGDPNGVNRFGRRAIQVMMGSGAR-VAELLLLHGAEPNCADP 76
| : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 577 HGNT-PLHVACKDGNFIVVALCEANCLNLSIKYIGTPTPLHLAANNGLDVRVL 530
| : : : : : | | | | | : : : : : | | | | | : : : : : |
Qy 77 ATLTPRVDAAREGEFLDTLVVHLRAGARLDVRDANGRLPVDLAERGRHVDVAGYL 131
| : : : : : | | | | | : : : : : | | | | | : : : : : |
RESULT 12
ID ANK1_HUMAN STANDARD; PRT; 1880 AA.
AC P16157;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).
GN ANK1 OR ANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A. PARTIAL SEQUENCE, AND VARIANTS.
RX TISSUE-HEMATOPOIETIC;
RX MEDLINE; 90158830.
RA Lux S.E., John K.M., Bennett V.;
RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
RT structure with homology to tissue-differentiation and cell-cycle
RT control proteins.";
RL Nature 344:36-42(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90175370.
RA Lambert S.C., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D.,
RA Cheung M.C., Kan Y.W., Palek J.;
RT "cDNA sequence for human erythrocyte ankyrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
RN [3]
RP VARIANT HS ILE-462.
RX MEDLINE; 96225450.
RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
RT "Ankyrin-1 mutations are a major cause of dominant and recessive
RT hereditary spherocytosis.";
RL Nat. Genet. 13:214-218(1996).
CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
CC NA-K ATPASE, TO THE LIMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTE ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
CC PLASMA MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY
CC ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
CC VARIANT 2.1.
CC -1- PTM: REGULATED BY PHOSPHORYLATION.
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
CC -1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE
CC HEREDITARY SPHEROCYTOSIS (HS).
CC -1- SIMILARITY: CONTAINS 24 ANK REPEATS.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

FT DISULFID 89 BY SIMILARITY.
FT DISULFID 106 BY SIMILARITY.
FT DISULFID 111 BY SIMILARITY.
FT DISULFID 130 BY SIMILARITY.
FT DISULFID 139 BY SIMILARITY.
FT DISULFID 145 BY SIMILARITY.
FT DISULFID 150 BY SIMILARITY.
FT DISULFID 167 BY SIMILARITY.
FT DISULFID 183 BY SIMILARITY.
FT DISULFID 188 BY SIMILARITY.
FT DISULFID 205 BY SIMILARITY.
FT DISULFID 221 BY SIMILARITY.
FT DISULFID 226 BY SIMILARITY.
FT DISULFID 244 BY SIMILARITY.
FT DISULFID 260 BY SIMILARITY.
FT DISULFID 265 BY SIMILARITY.
FT DISULFID 282 BY SIMILARITY.
FT DISULFID 298 BY SIMILARITY.
FT DISULFID 305 BY SIMILARITY.
FT DISULFID 322 BY SIMILARITY.
FT DISULFID 338 BY SIMILARITY.
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FT DISULFID 360 BY SIMILARITY.
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FT DISULFID 380 BY SIMILARITY.
FT DISULFID 399 BY SIMILARITY.
FT DISULFID 415 BY SIMILARITY.
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FT DISULFID 611 BY SIMILARITY.
FT DISULFID 628 BY SIMILARITY.
FT DISULFID 644 BY SIMILARITY.
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FT DISULFID 665 BY SIMILARITY.
FT DISULFID 681 BY SIMILARITY.
FT DISULFID 686 BY SIMILARITY.
FT DISULFID 703 BY SIMILARITY.
FT DISULFID 719 BY SIMILARITY.
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FT DISULFID 740 BY SIMILARITY.
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FT DISULFID 761 BY SIMILARITY.
FT DISULFID 778 BY SIMILARITY.
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FT DISULFID 832 BY SIMILARITY.
FT DISULFID 837 BY SIMILARITY.
FT DISULFID 856 BY SIMILARITY.
FT DISULFID 872 BY SIMILARITY.
FT DISULFID 877 BY SIMILARITY.
FT DISULFID 894 BY SIMILARITY.
FT DISULFID 910 BY SIMILARITY.
FT DISULFID 915 BY SIMILARITY.
FT DISULFID 932 BY SIMILARITY.
FT DISULFID 986 BY SIMILARITY.
FT DISULFID 991 BY SIMILARITY.
FT DISULFID 1008 BY SIMILARITY.
FT DISULFID 1024 BY SIMILARITY.
FT DISULFID 1029 BY SIMILARITY.
FT DISULFID 1046 BY SIMILARITY.

FT DISULFID 1062 BY SIMILARITY.
FT DISULFID 1067 BY SIMILARITY.
FT DISULFID 1084 BY SIMILARITY.
FT DISULFID 1100 BY SIMILARITY.
FT DISULFID 1121 BY SIMILARITY.
FT DISULFID 1130 BY SIMILARITY.
FT DISULFID 1141 BY SIMILARITY.
FT DISULFID 1159 BY SIMILARITY.
FT DISULFID 1168 BY SIMILARITY.
FT DISULFID 1170 BY SIMILARITY.
FT DISULFID 1179 BY SIMILARITY.
FT DISULFID 1186 BY SIMILARITY.
FT DISULFID 1191 BY SIMILARITY.
FT DISULFID 1208 BY SIMILARITY.
FT DISULFID 1224 BY SIMILARITY.
FT DISULFID 1237 BY SIMILARITY.
FT DISULFID 1254 BY SIMILARITY.
FT DISULFID 1270 BY SIMILARITY.
FT DISULFID 1275 BY SIMILARITY.
FT DISULFID 1294 BY SIMILARITY.
FT DISULFID 1310 BY SIMILARITY.
FT DISULFID 1315 BY SIMILARITY.
FT DISULFID 1335 BY SIMILARITY.
FT DISULFID 1351 BY SIMILARITY.
FT DISULFID 1356 BY SIMILARITY.
FT DISULFID 1373 BY SIMILARITY.
FT DISULFID 1390 BY SIMILARITY.
FT DISULFID 1395 BY SIMILARITY.
FT DISULFID 1414 BY SIMILARITY.
...
Note: remainder of annotations omitted.

Query Match 13.6%; Score 133; DB 1; Length 2524;
Best Local Similarity 33.6%; Pred. No. 3.72e-07;
Matches 38; Conservative 27; Mismatches 43; Indels 5; Gaps 5;

Db 1996 LILARLAVEGVEPILNAHADVNAVDFGKSAHWAANVNDAAVLLKNSANKD-MQ 2054
QY 18 LATPARGLVE-KVHSWEAGADPNGVNFGRRAIQ-VMMGSGARVAEALLLHGAEPCAD 75
Db 2055 NKKEETSLFLAAREGSYETAKVLLDHYANR-DITDHMDRLPRDIAQERMHDI 2106
QY 76 PATLTPVHDAAREGFLDTL-VLHHRAGARLDVRDAGRLPVDLAERGRHDV 127

RESULT 15
ID ANKC_HUMAN STANDARD; PRT; 1839 AA.
AC Q01485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)
DE (FRAGMENT).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN STEM;
RX MEDLINE; 91302466.
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114:241-253(1991).
RN [2]
RP SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE; 92009921.
RA Tse W.T., Menninger J.C., Yang-Peng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
RT ankyrin gene.";
RL Genomics 10:858-866(1991).
CC -1- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN

(TM)

Result No.	Query %		DB	ID	Description	Pred. No.
	Score	Match				
1	598	61.2	86	6	Q9X552	P15/MTS2/CDKN2B (FRAGM
2	586	60.0	115	4	Q16361	CELL CYCLE NEGATIVE RE
3	582	59.6	102	6	Q9X551	P16/CDKN2A/MTS1 (FRAGM
4	574	58.8	168	11	P97510	CYCLIN DEPENDENT KINAS
5	570	58.3	168	11	Q89088	CYCLIN DEPENDENT KINAS
6	563	57.6	86	11	Q9Z1C1	CYCLIN-DEPENDENT KINAS
7	551	56.4	86	11	Q54846	CYCLIN-DEPENDENT KINAS
8	479	49.0	113	11	Q9Z1C2	CYCLIN-DEPENDENT KINAS
9	368	37.3	134	13	P70067	CDKN2X PROTEIN.
10	358	36.6	58	6	Q97886	CYCLIN-DEPENDENT KINAS
11	357	36.5	124	13	Q9W618	P13CDKN2X.
12	309	31.6	78	4	Q15125	ALTERNATIVE SPLICED FO
13	186	19.0	44	11	Q9Z1C0	CYCLIN-DEPENDENT KINAS
14	141	14.4	745	4	Q9Y344	DZ0208.1 (NOVEL RAT E
15	140	14.3	1719	4	Q13768	ALT. ANKYRIN (VARIANT
16	140	14.3	1856	4	Q99407	ANKYRIN.
17	139	14.2	800	5	Q43988	HOMEBOX-CONTAINING PR
18	139	14.2	837	11	Q63518	ESPIN.
19	137	14.0	1098	11	Q61304	ANKYRIN 1, ERYTHROID (
20	137	14.0	1848	11	Q61302	ANKYRIN 1, ERYTHROID (

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA STONE S., JIANG P., DAYANANTH P., TAVTIGIAN S.V., KATCHER H.,
RA PARRY D., PETERS G., KAMB A.;
RA "Complex structure and regulation of the p16 (MTS1) locus.";
RT Cancer Res. 55:2988-2994(1995).
RL EMBL; S78535; AAC60650.1; -.
DR HSSP; P42771; 1B17.
FT NON_TER 1
SQ SEQUENCE 115 AA; 12334 MW; F5BEP54B CRC32;

Query Match 60.0%; Score 586; DB 4; Length 115;
Best Local Similarity 95.3%; Pred. No. 1.61e-100;
Matches 82; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 9 QVMMGSAVVAELLHGAEPNCPADPATITRPVHDAAREGFLDTLVVLRAGARLDVRDA 68
Qy 51 QVMMGSAVVAELLHGAEPNCPADPATITRPVHDAAREGFLDTLVVLRAGARLDVRDA 110
|||||
Db 69 WGRLPVDLAELGHRDVARVYRAAG 94
Qy 111 WGRLPVDLAELGHRDVARVYRAAG 136
|||||

RESULT 3
ID Q9XS51 PRELIMINARY; PRT; 102 AA.
AC Q9XS51;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE P16(CDKN2A/MTS1 (FRAGMENT))
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RA KISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
RA "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
RT submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010807; BAA33540.1; -.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 10824 MW; 8C3094E9 CRC32;

Query Match 59.6%; Score 582; DB 6; Length 102;
Best Local Similarity 92.9%; Pred. No. 1.24e-99;
Matches 79; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 1 VMMGSAVVAELLHGAEPNCPADPATITRPVHDAAREGFLDTLVVLRAGARLDVRDA 60
Qy 52 VMMGSAVVAELLHGAEPNCPADPATITRPVHDAAREGFLDTLVVLRAGARLDVRDA 111
|||||
Db 61 GRPLPVDLAELGHRDVARVYRAAG 85
Qy 112 GRPLPVDLAELGHRDVARVYRAAG 136
|||||

RESULT 4
ID P97510 PRELIMINARY; PRT; 168 AA.
AC P97510; P97937;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR
PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16, INHIBITS CDK4)
DE (P16INK4A) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
DE CDKN2A OR E1ALPHA OR P16INK4A OR CDKN2A.
GN

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-DBA/2N; TISSUE-SPLEEN;
RA MEDLINE; 98151529;
RA ZHANG S., RAMSAY E.S., MOCK B.A.;
RT "cdk2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
p19ARF, is a candidate for the plasmacytoma susceptibility locus,
Pctrl.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
RN [2]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RX MEDLINE; 97179476;
RA HERZOG C.R., YOU M.;
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
suppressor gene.";
RL Mamm. Genome 8:65-66(1997).
RN [3]
RP SEQUENCE OF 1-155 FROM N.A.
RC STRAIN-C57BL/6J X DBA;
RA MALUMBRES M., DE CASTRO I., SANTOS J., MELENDEZ B., MANGUES R.,
RA SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.;
RT submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-DBA/2 AND C57BL/6;
RX MEDLINE; 95380169;
RA QUELLE D.E., ASHMUN R.A., HANNON G.J., REHBERGER P.A., TRONO D.,
RA RICHTER K.H., WALKER C., BEACH D., SHERR C.J., SERRANO M.;
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
RN Oncogene 11:635-645(1995).
RN [5]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-DBA/2 AND C57BL/6;
RA GRESSANI K.M., ROLLINS L.A., MILLER M.S.;
RT submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN-ICR SWISS;
RX MEDLINE; 97128829;
RA SOLOFF E.V., HERZOG C.R., YOU M.;
RT "The 5'-flanking region of the E1 alpha form of the murine p16INK4a
(MTS1) gene.";
RL Gene 180:213-215(1996).
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RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-CAST/EI, C57BL/6J AND RF/J, MOLE/EI AND MUS MUSCULUS;
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
RA PELLICER A., FERNANDEZ-PIQUERAS J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044336; AAC08963.1; -.
DR EMBL; U49280; AAC00052.1; -.
DR EMBL; U66087; AAB39600.1; -.
DR EMBL; U66086; AAB39600.1; JOINED.
DR EMBL; AF004588; AAB61416.1; -.
DR EMBL; U47018; AAC52987.1; -.
DR EMBL; U79628; AAD00226.1; -.
DR EMBL; U79625; AAD00223.1; -.
DR EMBL; U79627; AAD00225.1; -.
DR HSSP; P42771; 1B17.
DR MGD; MGI-104738; Cdkn2a.
DR PFAM; PF00023; ank; 3.
RW Kinase; Cyclin.
SQ SEQUENCE 168 AA; 17941 MW; 89AD5E62 CRC32;

Query Match 58.8%; Score 574; DB 11; Length 168;
Best Local Similarity 65.0%; Pred. No. 7.35e-98;
Matches 80; Conservative 21; Mismatches 21; Indels 1; Gaps 1;

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